



1

## SEQUENCE LISTING

<110> University of Utah Research Foundation  
Cognetix, Inc.  
Jones, Robert M.  
Garrett, James E.  
Watkins, Maren  
Olivera, Baldomero M.

<120> B-Superfamily Conotoxins

<130> 2314-248

<140> US 10/058,053

<141> 2002-01-29

<150> US 60/264323

<151> 2001-01-29

<160> 340

<170> PatentIn version 3.0

<210> 1

<211> 456

<212> DNA

<213> Conus flavidus

<220>

<221> CDS

<222> (7)..(255)

<400> 1

ggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg 48  
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp  
1 5 10

att aca gcc cct ctg tct gaa ggt ggt aaa ttg aac gac gta att cgg 96  
Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg  
15 20 25 30

ggt ttg gtg cca gat gac tta acc cca cag ctt att ttg caa agt ctg 144  
Gly Leu Val Pro Asp Asp Leu Thr Pro Gln Leu Ile Leu Gln Ser Leu  
35 40 45

gat tcc cgt cgt cat gat cac ggc att cgt ccg aag aga gtc gac ata 192  
Asp Ser Arg Arg His Asp His Gly Ile Arg Pro Lys Arg Val Asp Ile  
50 55 60

tgt aac tgg agg ata tgt gca cca aac cca ttg aga cga cat gat ctt 240  
Cys Asn Trp Arg Ile Cys Ala Pro Asn Pro Leu Arg Arg His Asp Leu  
65 70 75

aag aaa gga aac aat tgacgtcaga caaccgccac aacttgagta cgacatcggt 295  
Lys Lys Gly Asn Asn  
80

aatacgactt cagcaaatat gaaattttca gcatcactgt gggtgtgaag aaatcagttg 355

ctttaaaagg ttggatttgt ccttggtttaa gccgttgtac tgatgacatc tctgcactat 415

gaaataaagc tgatgtgaca aactaaaaaa aaaaaaaaaa a

456

<210> 2  
 <211> 83  
 <212> PRT  
 <213> Conus flavidus

<400> 2  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15  
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu  
 20 25 30  
 Val Pro Asp Asp Leu Thr Pro Gln Leu Ile Leu Gln Ser Leu Asp Ser  
 35 40 45  
 Arg Arg His Asp His Gly Ile Arg Pro Lys Arg Val Asp Ile Cys Asn  
 50 55 60  
 Trp Arg Ile Cys Ala Pro Asn Pro Leu Arg Arg His Asp Leu Lys Lys  
 65 70 75 80

Gly Asn Asn

<210> 3  
 <211> 33  
 <212> PRT  
 <213> Conus flavidus

<220>  
 <221> PEPTIDE  
 <222> (1)..(33)  
 <223> Xaa at residues 7, 20 and 22 may be Pro or hydroxy-Pro; Xaa at re  
 sidue 15 may be Trp (Dor L) or bromo-Trp (Dor L)

<400> 3  
 His Asp His Gly Ile Arg Xaa Lys Arg Val Asp Ile Cys Asn Xaa Arg  
 1 5 10 15  
 Ile Cys Ala Xaa Asn Xaa Leu Arg Arg His Asp Leu Lys Lys Gly Asn  
 20 25 30

Asn

<210> 4  
 <211> 374  
 <212> DNA  
 <213> Conus miles

<220>  
 <221> CDS  
 <222> (7)..(315)

<400> 4  
 ggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg gtg  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Val  
 1 5 10

48

## 3

ggg ctc acc gtc ggg agt cac gtc cat cgg tct cac agt cct aca tcg 96  
 Gly Leu Thr Val Gly Ser His Val His Arg Ser His Ser Pro Thr Ser  
 15 20 25 30

cgc agc cat ggt gat gac tcc att cat gac aag acg att cat caa cat 144  
 Arg Ser His Gly Asp Asp Ser Ile His Asp Lys Thr Ile His Gln His  
 35 40 45

ctg ttt gcc cgt ctt cct ctg gag aac aac gac gac cat cgt tct gtg 192  
 Leu Phe Ala Arg Leu Pro Leu Glu Asn Asn Asp Asp His Arg Ser Val  
 50 55 60

gat ctt cct gca ggg aat ggt gca ggc aac acc aag caa caa gac caa 240  
 Asp Leu Pro Ala Gly Asn Gly Ala Gly Asn Thr Lys Gln Gln Asp Gln  
 65 70 75

agt cct cat cat gtg tgt tgt gct att ggt ccg gtt ctt cca ttc tgt 288  
 Ser Pro His His Val Cys Cys Ala Ile Gly Pro Val Leu Pro Phe Cys  
 80 85 90

tgt gtc agt tgg ctg cac aaa ctc cat tgaactggcc aatgaaaata 335  
 Cys Val Ser Trp Leu His Lys Leu His  
 95 100

actcaggaat agacagaaag gcaaaaaaaaa aaaaaaaaaa 374

<210> 5  
 <211> 103  
 <212> PRT  
 <213> Conus miles

<400> 5  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Val Gly Leu  
 1 5 10 15

Thr Val Gly Ser His Val His Arg Ser His Ser Pro Thr Ser Arg Ser  
 20 25 30

His Gly Asp Asp Ser Ile His Asp Lys Thr Ile His Gln His Leu Phe  
 35 40 45

Ala Arg Leu Pro Leu Glu Asn Asn Asp Asp His Arg Ser Val Asp Leu  
 50 55 60

Pro Ala Gly Asn Gly Ala Gly Asn Thr Lys Gln Gln Asp Gln Ser Pro  
 65 70 75 80

His His Val Cys Cys Ala Ile Gly Pro Val Leu Pro Phe Cys Cys Val  
 85 90 95

Ser Trp Leu His Lys Leu His  
 100

<210> 6  
 <211> 29  
 <212> PRT  
 <213> Conus miles

<220>  
 <221> PEPTIDE

<222> (1)..(29)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residues 6, 15 and 18 may be Pro or hydroxy-Pro; Xaa at residue 24 may be Trp (D or L) or bromo-Trp (D or L)

<400> 6

Xaa Gln Asp Gln Ser Xaa His His Val Cys Cys Ala Ile Gly Xaa Val  
1 5 10 15

Leu Xaa Phe Cys Cys Val Ser Xaa Leu His Lys Leu His  
20 25

<210> 7

<211> 359

<212> DNA

<213> Conus miles

<220>

<221> CDS

<222> (7)..(291)

<400> 7

ggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg gtg 48  
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Val  
1 5 10

ggg ttc acc gtc ggg ggt cac gtc cat cgg tct cac agt cct aca tcg 96  
Gly Phe Thr Val Gly Gly His Val His Arg Ser His Ser Pro Thr Ser  
15 20 25 30

cgc agc cat ggt gat gac tcc att cat gac aag acg att cat caa cat 144  
Arg Ser His Gly Asp Asp Ser Ile His Asp Lys Thr Ile His Gln His  
35 40 45

ctg ttt gcc cgt ctt cct cag gag aac aac gac gac cat cgt tct gtg 192  
Leu Phe Ala Arg Leu Pro Gln Glu Asn Asn Asp Asp His Arg Ser Val  
50 55 60

gat ctt cct gca ggg act agc gca ggc gac atg aaa cca caa cgc caa 240  
Asp Leu Pro Ala Gly Thr Ser Ala Gly Asp Met Lys Pro Gln Arg Gln  
65 70 75

aga cgt ctc tgc tgc atc ttt gcc ccg att ctt tgg ttc tgt tgt cac 288  
Arg Arg Leu Cys Cys Ile Phe Ala Pro Ile Leu Trp Phe Cys Cys His  
80 85 90

ggg taacagctca aattacactg cactggccga ttgaaagaac tgcaataaac 341  
Gly  
95

ggaaaaaaaa aaaaaaaaaa 359

<210> 8

<211> 95

<212> PRT

<213> Conus miles

<400> 8

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Val Gly Phe  
1 5 10 15

Thr Val Gly Gly His Val His Arg Ser His Ser Pro Thr Ser Arg Ser  
                   20                  25                  30  
 His Gly Asp Asp Ser Ile His Asp Lys Thr Ile His Gln His Leu Phe  
                   35                  40                  45  
 Ala Arg Leu Pro Gln Glu Asn Asn Asp Asp His Arg Ser Val Asp Leu  
                   50                  55                  60  
 Pro Ala Gly Thr Ser Ala Gly Asp Met Lys Pro Gln Arg Gln Arg Arg  
                   65                  70                  75                  80  
 Leu Cys Cys Ile Phe Ala Pro Ile Leu Trp Phe Cys Cys His Gly  
                   85                  90                  95

<210> 9

<211> 14

<212> PRT

<213> Conus miles

<220>

<221> PEPTIDE

<222> (1)..(14)

<223> Xaa at residue 7 may be Pro or hydroxy-Pro; Xaa at residue 10 may  
 be Trp (D or L) or bromo-Trp (D or L)

<400> 9

Leu Cys Cys Ile Phe Ala Xaa Ile Leu Xaa Phe Cys Cys His  
 1                  5                  10

<210> 10

<211> 351

<212> DNA

<213> Conus capitaneus

<220>

<221> CDS

<222> (7)..(291)

<400> 10

ggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg gtg 48  
           Met Gln Thr Ala Tyr Trp Val Met Val Met Met Val Val  
           1                  5                  10

ggg ttc acc gtc ggg ggt cac gtc cat cgg tct cac agt cct aca tcg 96  
           Gly Phe Thr Val Gly Gly His Val His Arg Ser His Ser Pro Thr Ser  
           15                  20                  25                  30

cgc agc cat ggt gat gac tcc att cat gac gag acg att cat caa cat 144  
           Arg Ser His Gly Asp Asp Ser Ile His Asp Glu Thr Ile His Gln His  
                   35                  40                  45

ctg ttt gcc cgt ctt cct cag gag aac aac gac gac cat cgt tct gtg 192  
           Leu Phe Ala Arg Leu Pro Gln Glu Asn Asn Asp Asp His Arg Ser Val  
                   50                  55                  60

gat ctt cct gca ggg act agc gca ggc gac atg aaa cca caa cgc caa 240  
           Asp Leu Pro Ala Gly Thr Ser Ala Gly Asp Met Lys Pro Gln Arg Gln  
                   65                  70                  75

aga ggt ttc tgc tgc gac ttt ccc ccg att ttt tgg ttc tgt tgt atc 288  
 Arg Gly Phe Cys Cys Asp Phe Pro Pro Ile Phe Trp Phe Cys Cys Ile  
 80 85 90

ggt taacagcaca aattacactg cactggccga ttgaaagaac tgcaataaac 341  
 Gly  
 95

ggaaaaaaaaa 351

<210> 11  
 <211> 95  
 <212> PRT  
 <213> Conus capitaneus

<400> 11  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Val Gly Phe  
 1 5 10 15

Thr Val Gly Gly His Val His Arg Ser His Ser Pro Thr Ser Arg Ser  
 20 25 30

His Gly Asp Asp Ser Ile His Asp Glu Thr Ile His Gln His Leu Phe  
 35 40 45

Ala Arg Leu Pro Gln Glu Asn Asn Asp Asp His Arg Ser Val Asp Leu  
 50 55 60

Pro Ala Gly Thr Ser Ala Gly Asp Met Lys Pro Gln Arg Gln Arg Gly  
 65 70 75 80

Phe Cys Cys Asp Phe Pro Pro Ile Phe Trp Phe Cys Cys Ile Gly  
 85 90 95

<210> 12  
 <211> 15  
 <212> PRT  
 <213> Conus capitaneus

<220>  
 <221> PEPTIDE  
 <222> (1)..(15)  
 <223> Xaa at residues 7 and 8 may be Pro or hydroxy-Pro; Xaa at residue  
 11 may be Trp (D or L) or bromo-Trp (D or L)

<400> 12  
 Gly Phe Cys Cys Asp Phe Xaa Xaa Ile Phe Xaa Phe Cys Cys Ile  
 1 5 10 15

<210> 13  
 <211> 348  
 <212> DNA  
 <213> Conus generalis

<220>  
 <221> CDS  
 <222> (7)..(222)

<400> 13  
 ggatcc atg cag acg gcc tac tgg gta atg gtg atg atg atg gtg tgg 48

[illegible]

<210> 16  
 <211> 405  
 <212> DNA  
 <213> Conus wittigi

<220>  
 <221> CDS  
 <222> (1)..(210)

<220>  
 <221> misc\_feature  
 <222> (1)..(405)  
 <223> n may be any base

<400> 16  
 atg atg ttg gtg tgg att aca gcc cct ctg cct gaa ggt ggt aaa ctg 48  
 Met Met Leu Val Trp Ile Thr Ala Pro Leu Pro Glu Gly Gly Lys Leu  
 1 5 10 15  
 aag cac gta att cgg ggt ttg gtg cca gac gac tta acc cca cag ctt 96  
 Lys His Val Ile Arg Gly Leu Val Pro Asp Asp Leu Thr Pro Gln Leu  
 20 25 30  
 atc ttg cga agt ctg att tcc cgt cgt agt tct gac ggc agt gat ccg 144  
 Ile Leu Arg Ser Leu Ile Ser Arg Arg Ser Ser Asp Gly Ser Asp Pro  
 35 40 45  
 aag gca aaa aaa cag tgt atg tgg aag aga tgt ata cca gac caa tcg 192  
 Lys Ala Lys Lys Gln Cys Met Trp Lys Arg Cys Ile Pro Asp Gln Ser  
 50 55 60  
 aga cta gaa gaa gat gaa tgatgtcaga caaccgccat cactgtagta 240  
 Arg Leu Glu Glu Asp Glu  
 65 70  
 tgacatcggtt aatacgactt aagcaaatat tttacatca ctgtgggttct gaagacatca 300  
 gttgcttttaa aagattggat tcttccttgt ttaagagttg tactganatc attcctgccc 360  
 tgtgaaataa agctgatgtt gacanncaaa caaaaaaaaa aaaaa 405

<210> 17  
 <211> 70  
 <212> PRT  
 <213> Conus wittigi

<400> 17  
 Met Met Leu Val Trp Ile Thr Ala Pro Leu Pro Glu Gly Gly Lys Leu  
 1 5 10 15  
 Lys His Val Ile Arg Gly Leu Val Pro Asp Asp Leu Thr Pro Gln Leu  
 20 25 30  
 Ile Leu Arg Ser Leu Ile Ser Arg Arg Ser Ser Asp Gly Ser Asp Pro  
 35 40 45  
 Lys Ala Lys Lys Gln Cys Met Trp Lys Arg Cys Ile Pro Asp Gln Ser  
 50 55 60



Arg Leu Glu Glu Asp Glu  
65 70

<210> 18  
<211> 29  
<212> PRT  
<213> Conus wittigi

<220>  
<221> PEPTIDE  
<222> (1)..(29)  
<223> Xaa at residues 7 and 20 may be Pro or hydroxy-Pro; Xaa at residue 15 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 26, 27 and 29 may be Glu or Gla

<400> 18  
Ser Ser Asp Gly Ser Asp Xaa Lys Ala Lys Lys Gln Cys Met Xaa Lys  
1 5 10 15

Arg Cys Ile Xaa Asp Gln Ser Arg Leu Xaa Xaa Asp Xaa  
20 25

<210> 19  
<211> 463  
<212> DNA  
<213> Conus consors

<220>  
<221> CDS  
<222> (7)..(222)

<400> 19  
ggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg 48  
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp  
1 5 10

att aca gcc cct ctg tct gaa ggt ggt aaa ttg aac gac gta att cgg 96  
Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg  
15 20 25 30

ggt ttg gtg tca cac atc tta atc cca cag cat acc ttg cga agt ctg 144  
Gly Leu Val Ser His Ile Leu Ile Pro Gln His Thr Leu Arg Ser Leu  
35 40 45

act tcc cgt gat cgt tct gac aac ggt ggt tcg agt gga gca caa ata 192  
Thr Ser Arg Asp Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile  
50 55 60

tgc atc tgg aag gta tgt cca cca tcc cca tagagacgac cacgaggaaa 242  
Cys Ile Trp Lys Val Cys Pro Pro Ser Pro  
65 70

aagatgaacg gcgtcagaca accgccacaa ctgtagtacg acatcggttga tacgacttca 302

gcaactatatt taacatcact gtggttgtga agaaatcagt cgcttttaaaa gattggattt 362

ttccttgttt aagagttgta ctgatatcag ctctgcacta tgaaataaag ctgatgtgac 422

ataaaaaaaaa aaaaaaaaaag tactctgcgt tgttactcga g 463

<210> 20  
 <211> 72  
 <212> PRT  
 <213> Conus consors

<400> 20  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15  
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu  
 20 25 30  
 Val Ser His Ile Leu Ile Pro Gln His Thr Leu Arg Ser Leu Thr Ser  
 35 40 45  
 Arg Asp Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile  
 50 55 60  
 Trp Lys Val Cys Pro Pro Ser Pro  
 65 70

<210> 21  
 <211> 23  
 <212> PRT  
 <213> Conus consors

<220>  
 <221> PEPTIDE  
 <222> (1)..(23)  
 <223> Xaa at residue 16 may be Trp (D or L) or bromo-Trp (D or L); Xaa  
 at residues 20, 21 and 23 may be Pro or hydroxy-Pro

<400> 21  
 Asp Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile Xaa  
 1 5 10 15  
 Lys Val Cys Xaa Xaa Ser Xaa  
 20

<210> 22  
 <211> 470  
 <212> DNA  
 <213> Conus consors

<220>  
 <221> CDS  
 <222> (7)..(246)

<400> 22  
 ggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg 48  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp  
 1 5 10  
 att aca gcc cct ctg tct gaa ggt ggt aaa ttg aac gac gca att cgg 96  
 Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Ala Ile Arg  
 15 20 25 30  
 ggt ttg gtg tca cac atc tta atc cca cag cat acc ttg cga agt ctg 144  
 Gly Leu Val Ser His Ile Leu Ile Pro Gln His Thr Leu Arg Ser Leu  
 35 40 45

act tcc cgt gct cgt tct gac aac ggt ggt tcg agt gga gca caa ata 192  
 Thr Ser Arg Ala Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile  
                   50                                  55                                  60

tgc atc tgg aag gta tgt cca cca tcc cca tgg aga cga cca caa gga 240  
 Cys Ile Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Arg Pro Gln Gly  
                   65                                  70                                  75

aaa aga tgaatgacgt cagacaaccg ccacaactgt agtacgacat cggttgatacg 296  
 Lys Arg  
           80

acttcagcaa atattttaac atcactgtgg ttgtgaagaa atcagttgct ttaaaagatt 356

ggatttttcc ttgtttaaga gttgtactga tatcagctct gcactatgaa ataaagctga 416

tgtgacaaac aataaaaaag aaaaaaaaaa aagtactctg cgttgttact cgag 470

<210> 23

<211> 80

<212> PRT

<213> Conus consors

<400> 23

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1                  5                                  10                                  15

Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Ala Ile Arg Gly Leu  
                   20                                  25                                  30

Val Ser His Ile Leu Ile Pro Gln His Thr Leu Arg Ser Leu Thr Ser  
                   35                                  40                                  45

Arg Ala Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile  
                   50                                  55                                  60

Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Arg Pro Gln Gly Lys Arg  
 65                                  70                                  75                                  80

<210> 24

<211> 28

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residues 16 and 24 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 20, 21, 23 and 27 may be Pro or hydroxy-Pro

<400> 24

Ala Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile Xaa  
 1                  5                                  10                                  15

Lys Val Cys Xaa Xaa Ser Xaa Xaa Arg Arg Xaa Gln  
                   20                                  25

<210> 25

<211> 469

<212> DNA  
 <213> Conus consors

<220>  
 <221> CDS  
 <222> (7)..(228)

<400> 25  
 ggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg 48  
           Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp  
           1                  5                  10

att aca gcc cct ctg tct gaa ggt ggt aaa ttg aac gac gta att cgg 96  
 Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg  
 15                  20                  25                  30

ggt ttg gtg cca cac ttc tta acc cca cag cat atc ttg caa agt ctg 144  
 Gly Leu Val Pro His Phe Leu Thr Pro Gln His Ile Leu Gln Ser Leu  
                   35                  40                  45

act tcc cgt aat ggt tct ggc agc agt aat cag aaa gaa gca caa cta 192  
 Thr Ser Arg Asn Gly Ser Gly Ser Ser Asn Gln Lys Glu Ala Gln Leu  
                   50                  55                  60

tgc atc tgg aag gta tgt cca cca tcc cca tgg aga tgaccacaag 238  
 Cys Ile Trp Lys Val Cys Pro Pro Ser Pro Trp Arg  
           65                  70

gaaaaagatg aacggcgtca gacaaccgcc acaactgtag tgggacatcg ttgatacgac 298

ttcagcaaat attttaacat cactgtgggt gtgaagaaat cagttgcttt aaaagattgg 358

atttttcctt gtttaagaat tgtactgata tcagctctgc actatgaaat aaagctgatg 418

tgacaaccca aaaaaaaaaa aaaaaaaaaag tactctgcg\_\_tggtactcga g 469

<210> 26  
 <211> 74  
 <212> PRT  
 <213> Conus consors

<400> 26  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1                  5                  10                  15

Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu  
           20                  25                  30

Val Pro His Phe Leu Thr Pro Gln His Ile Leu Gln Ser Leu Thr Ser  
           35                  40                  45

Arg Asn Gly Ser Gly Ser Ser Asn Gln Lys Glu Ala Gln Leu Cys Ile  
           50                  55                  60

Trp Lys Val Cys Pro Pro Ser Pro Trp Arg  
 65                  70

<210> 27  
 <211> 25  
 <212> PRT

<213> Conus consors

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 10 may be Glu or Gla; Xaa at residues 16 and 24 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 20, 21 and 23 may be Pro or hydroxy-Pro

<400> 27  
 Asn Gly Ser Gly Ser Ser Asn Gln Lys Xaa Ala Gln Leu Cys Ile Xaa  
 1 5 10 15

Lys Val Cys Xaa Xaa Ser Xaa Xaa Arg  
 20 25

<210> 28  
 <211> 472  
 <212> DNA  
 <213> Conus tulipa

<220>  
 <221> CDS  
 <222> (7)..(231)

<220>  
 <221> misc\_feature  
 <222> (1)..(472)  
 <223> n may be any base

<400> 28  
 ggatcc atg cag acg gcc tac tgg gtg atg ctg atg atg atg gtg tgg 48  
 Met Gln Thr Ala Tyr Trp Val Met Leu Met Met Met Val Trp  
 1 5 10

att aca gcc cct ctg tct gaa ggt ggt aaa ctg aac gac gta att cgg 96  
 Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg  
 15 20 25 30

ggt ttg gtg cca cac gtc tta acc cca cag cat atc ttg caa agt ctg 144  
 Gly Leu Val Pro His Val Leu Thr Pro Gln His Ile Leu Gln Ser Leu  
 35 40 45

gtt tcc cgt cgt cat ttt aac agc gtt gtt ccg acg gta tac ata tgc 192  
 Val Ser Arg Arg His Phe Asn Ser Val Val Pro Thr Val Tyr Ile Cys  
 50 55 60

atg tgg aag gta tgt cca cca tcg cca tag aga cga cca taaggaaaaa 241  
 Met Trp Lys Val Cys Pro Pro Ser Pro Arg Arg Pro  
 65 70

gatgaatgac gtcagacaac cgccacaact gtagtacgac atcgттаата cgacttcagc 301

aaatatttta acatcactgt ggttgtgaag aaatcagttg ctttaaaaga ttggattttt 361

ccttgttttca gagttgtact gatatcagct ctgcactatc aaataaagct gaagtgcaca 421

accnnaaaaa aaaaaaaaaa aaaaaaaaag tactctgcgt tgttactcga g 472

<210> 29  
 <211> 71

&lt;212&gt; PRT

&lt;213&gt; Conus tulipa

&lt;400&gt; 29

Met	Gln	Thr	Ala	Tyr	Trp	Val	Met	Leu	Met	Met	Met	Val	Trp	Ile	Thr
1				5				10						15	

Ala	Pro	Leu	Ser	Glu	Gly	Gly	Lys	Leu	Asn	Asp	Val	Ile	Arg	Gly	Leu
			20					25					30		

Val	Pro	His	Val	Leu	Thr	Pro	Gln	His	Ile	Leu	Gln	Ser	Leu	Val	Ser
		35					40					45			

Arg	Arg	His	Phe	Asn	Ser	Val	Val	Pro	Thr	Val	Tyr	Ile	Cys	Met	Trp
	50					55					60				

Lys	Val	Cys	Pro	Pro	Ser	Pro
65					70	

&lt;210&gt; 30

&lt;211&gt; 21

&lt;212&gt; PRT

&lt;213&gt; Conus tulipa

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(21)

<223> Xaa at residues 7, 18, 19 and 21 may be Pro or hydroxy-Pro; Xaa at residue 10 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Trp or bromo-Trp

&lt;400&gt; 30

His	Phe	Asn	Ser	Val	Val	Xaa	Thr	Val	Xaa	Ile	Cys	Met	Xaa	Lys	Val
1				5					10					15	

Cys	Xaa	Xaa	Ser	Xaa
			20	

&lt;210&gt; 31

&lt;211&gt; 451

&lt;212&gt; DNA

&lt;213&gt; Conus tulipa

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(279)

&lt;400&gt; 31

atg	cag	acg	gcc	tac	tgg	gtg	atg	ctg	ttg	atg	atg	gtg	ggc	att	aca	48
Met	Gln	Thr	Ala	Tyr	Trp	Val	Met	Leu	Leu	Met	Met	Val	Gly	Ile	Thr	
1				5				10						15		

gcc	cct	ctg	cct	gaa	ggg	ggg	aaa	ccg	aac	agc	gta	att	cgg	ggg	ttg	96
Ala	Pro	Leu	Pro	Glu	Gly	Gly	Lys	Pro	Asn	Ser	Val	Ile	Arg	Gly	Leu	
			20					25					30			

gtg	cca	aac	gac	tta	act	cca	cag	cat	acc	ttg	cga	agt	ctg	att	tcc	144
Val	Pro	Asn	Asp	Leu	Thr	Pro	Gln	His	Thr	Leu	Arg	Ser	Leu	Ile	Ser	
		35					40					45				

cgt cgt caa act gac gtt ctt ctg gag gct acc ctt ttg aca aca cca 192  
 Arg Arg Gln Thr Asp Val Leu Leu Glu Ala Thr Leu Leu Thr Thr Pro  
           50                              55                              60

gcc ccc gag cag aga ttg ttc tgc ttc tgg aag tca tgt tgg cca agg 240  
 Ala Pro Glu Gln Arg Leu Phe Cys Phe Trp Lys Ser Cys Trp Pro Arg  
           65                              70                              75                              80

ccc tac cct tgg aga cga cgt gat ctt aat gga aaa cga tgaatgacgt 289  
 Pro Tyr Pro Trp Arg Arg Arg Asp Leu Asn Gly Lys Arg  
                               85                              90

cagacaaccg ccacaactgt agtacgacat cattaatacg acttcagcaa atattttaac 349

attactgtgg ttgtgaagaa atcacttgct ttaaaagatt ggttttttcc ttgtttcaga 409

gttggtactga tatcagctct gccctatgaa ataaagctga tg 451

<210> 32

<211> 93

<212> PRT

<213> Conus tulipa

<400> 32

Met Gln Thr Ala Tyr Trp Val Met Leu Leu Met Met Val Gly Ile Thr  
 1                              5                              10                              15

Ala Pro Leu Pro Glu Gly Gly Lys Pro Asn Ser Val Ile Arg Gly Leu  
           20                              25                              30

Val Pro Asn Asp Leu Thr Pro Gln His Thr Leu Arg Ser Leu Ile Ser  
           35                              40                              45

Arg Arg Gln Thr Asp Val Leu Leu Glu Ala Thr Leu Leu Thr Thr Pro  
           50                              55                              60

Ala Pro Glu Gln Arg Leu Phe Cys Phe Trp Lys Ser Cys Trp Pro Arg  
           65                              70                              75                              80

Pro Tyr Pro Trp Arg Arg Arg Asp Leu Asn Gly Lys Arg  
                               85                              90

<210> 33

<211> 40

<212> PRT

<213> Conus tulipa

<220>

<221> PEPTIDE

<222> (1)..(40)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 7 and 17 may  
 be Glu or Gla; Xaa at residue 14, 16, 29, 31 and 33 may be Pro or  
 hydroxy-Pro; Xaa at residues 24, 28 and 34 may be Trp (D or L) o  
 r bromo-Trp (D or L)

<220>

<221> PEPTIDE

<222> (1)..(40)

<223> Xaa at residue 32 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Ty

r, O-sulpho-Tyr or O-phospho-Tyr

<400> 33

Xaa Thr Asp Val Leu Leu Xaa Ala Thr Leu Leu Thr Thr Xaa Ala Xaa  
1 5 10 15

Xaa Gln Arg Leu Phe Cys Phe Xaa Lys Ser Cys Xaa Xaa Arg Xaa Xaa  
20 25 30

Xaa Xaa Arg Arg Arg Asp Leu Asn  
35 40

<210> 34

<211> 414

<212> DNA

<213> *Conus sulcatus*

<220>

<221> CDS

<222> (1)..(285)

<400> 34

atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48  
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
1 5 10 15

gcc cct ctg tct gaa ggt ggt aaa ccg aac gac gta att cgg ggt ttg 96  
Ala Pro Leu Ser Glu Gly Gly Lys Pro Asn Asp Val Ile Arg Gly Leu  
20 25 30

gtg cca gac gac tta acc cca cag cgt gtc ttg cga agt ctg att tcc 144  
Val Pro Asp Asp Leu Thr Pro Gln Arg Val Leu Arg Ser Leu Ile Ser  
35 40 45

cgt cgt caa tct ggc tgc aga gtc ccg ttt gaa ttg aaa tgc atc tgg 192  
Arg Arg Gln Ser Gly Cys Arg Val Pro Phe Glu Leu Lys Cys Ile Trp  
50 55 60

aag ttc tgt aca ata tac cca tcg aga cca ttt gct tct ctg gaa gaa 240  
Lys Phe Cys Thr Ile Tyr Pro Ser Arg Pro Phe Ala Ser Leu Glu Glu  
65 70 75 80

aaa gac gaa tgt cag aca gtc acc ata act gta aca tgg gat ttt 285  
Lys Asp Glu Cys Gln Thr Val Thr Ile Thr Val Thr Trp Asp Phe  
85 90 95

taatacgtct ccagcaagta ttttaacatc actgtggttg tgaagaaatc agttgcttta 345

aaagattgga tttttccttg tttaagagtt gtactgatat cagctctgcc ctgtgaaata 405

aagctgatg 414

<210> 35

<211> 95

<212> PRT

<213> *Conus sulcatus*

<400> 35

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
1 5 10 15



Ala Pro Leu Ser Glu Gly Gly Lys Pro Asn Asp Val Ile Arg Gly Leu  
20 25 30

Val Pro Asp Asp Leu Thr Pro Gln Arg Val Leu Arg Ser Leu Ile Ser  
35 40 45

Arg Arg Gln Ser Gly Cys Arg Val Pro Phe Glu Leu Lys Cys Ile Trp  
50 55 60

Lys Phe Cys Thr Ile Tyr Pro Ser Arg Pro Phe Ala Ser Leu Glu Glu  
65 70 75 80

Lys Asp Glu Cys Gln Thr Val Thr Ile Thr Val Thr Trp Asp Phe  
85 90 95

<210> 36

<211> 45

<212> PRT

<213> Conus sulcatus

<220>

<221> PEPTIDE

<222> (1)..(45)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residues 7, 21 and 24 may be Pro or hydroxy-Pro; Xaa at residues 9, 29, 30 and 33 may be Glu or Gla; Xaa at residues 14 and 43 may be Trp (D or L) or bromo-Trp (D or L)

<220>

<221> PEPTIDE

<222> (1)..(45)

<223> Xaa at residue 20 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 36

Xaa Ser Gly Cys Arg Val Xaa Phe Xaa Leu Lys Cys Ile Xaa Lys Phe  
1 5 10 15

Cys Thr Ile Xaa Xaa Ser Arg Ser Phe Ala Ser Leu Xaa Xaa Lys Asp  
20 25 30

Xaa Cys Gln Thr Val Thr Ile Thr Val Thr Xaa Asp Phe  
35 40 45

<210> 37

<211> 413

<212> DNA

<213> Conus sulcatus

<220>

<221> CDS

<222> (1)..(234)

<400> 37

atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48  
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
1 5 10 15

gcc tct ctg tct gaa ggt ggt aaa ccg aac gac gtc att cgg ggt ttt 96

Ala Ser Leu Ser Glu Gly Gly Lys Pro Asn Asp Val Ile Arg Gly Phe  
20 25 30

gtg cca gac gac tta acc cca cag ctt atc ttg cga agt ctg att tcc 144  
Val Pro Asp Asp Leu Thr Pro Gln Leu Ile Leu Arg Ser Leu Ile Ser  
35 40 45

cgt cgt cgt tct gac aag gat gtt ggg aag aga atg gaa tgt tac tgg 192  
Arg Arg Arg Ser Asp Lys Asp Val Gly Lys Arg Met Glu Cys Tyr Trp  
50 55 60

aag gca tgt aga ccc acg cta tcg aga cga cat gat ctt ggg 234  
Lys Ala Cys Arg Pro Thr Leu Ser Arg Arg His Asp Leu Gly  
65 70 75

taaaagatga atgacgtcag acaacagcca caactatagt atgacatcgt taatacgact 294

tcagcaaata ttttaacatc actgtggttg tgaagaaatc agttgcttta aaagattgga 354

tttttcogtg ttttaagagtt gtactgatat cagctctgcc ctgtgaaata aagctgatg 413  
<210> 38  
<211> 78  
<212> PRT  
<213> Conus sulcatus

<400> 38  
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
1 5 10 15

Ala Ser Leu Ser Glu Gly Gly Lys Pro Asn Asp Val Ile Arg Gly Phe  
20 25 30

Val Pro Asp Asp Leu Thr Pro Gln Leu Ile Leu Arg Ser Leu Ile Ser  
35 40 45

Arg Arg Arg Ser Asp Lys Asp Val Gly Lys Arg Met Glu Cys Tyr Trp  
50 55 60

Lys Ala Cys Arg Pro Thr Leu Ser Arg Arg His Asp Leu Gly  
65 70 75

<210> 39  
<211> 27  
<212> PRT  
<213> Conus sulcatus

<220>  
<221> PEPTIDE  
<222> (1)..(27)  
<223> Xaa at residue 11 may be Glu or Gla; Xaa at residue 13 may be Pro  
or hydroxy-Pro; Xaa at residue 14 may be Trp (D or L) or bromo-T  
rp (D or L); Xaa at residue 19 may be Tyr, 125I-Tyr, mono-iodo-Ty  
r, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 39  
Arg Ser Asp Lys Asp Val Gly Lys Arg Met Xaa Cys Xaa Xaa Lys Ala  
1 5 10 15

Cys Arg Xaa Thr Leu Ser Arg Arg His Asp Leu  
20 25

<210> 40  
 <211> 451  
 <212> DNA  
 <213> Conus magus

<220>  
 <221> CDS  
 <222> (1)..(279)

<400> 40  
 atg cag acg gcc tac tgg gtg atg ctg atg atg atg gtg tgc atc aca 48  
 Met Gln Thr Ala Tyr Trp Val Met Leu Met Met Met Val Cys Ile Thr  
 1 5 10 15  
 gcc cct ctg cct gaa ggt ggt aaa ccg aac agc gga att cgg ggt ttg 96  
 Ala Pro Leu Pro Glu Gly Gly Lys Pro Asn Ser Gly Ile Arg Gly Leu  
 20 25 30  
 gtg cca aac gac tta act cca cag cat acc ttg cga agt ctg att tcc 144  
 Val Pro Asn Asp Leu Thr Pro Gln His Thr Leu Arg Ser Leu Ile Ser  
 35 40 45  
 cgt cgt caa act gac gtt ctt ctg gat gct acc ctt ttg aca aca cca 192  
 Arg Arg Gln Thr Asp Val Leu Leu Asp Ala Thr Leu Leu Thr Thr Pro  
 50 55 60  
 gcc ccc gag cag aga ttg ttc tgc ttc tgg aag tca tgt tgg cca agg 240  
 Ala Pro Glu Gln Arg Leu Phe Cys Phe Trp Lys Ser Cys Trp Pro Arg  
 65 70 75 80  
 ccc tac cct tgg aga cga cgt aat ctt aat gga aaa cga tgaatgacgt 289  
 Pro Tyr Pro Trp Arg Arg Arg Asn Leu Asn Gly Lys Arg  
 85 90  
 cagacaaccg ccacaactgt agtaacgacat cgттаатacg acttcagcaa atattttaac 349  
 ataactgtgg ttgtgaagaa atcggttgct ttaaaagatt ggatttttcc ttgtttcaga 409  
 gttgtactga tatgagctct gccctgtgaa ataaagctga tg 451

<210> 41  
 <211> 93  
 <212> PRT  
 <213> Conus magus

<400> 41  
 Met Gln Thr Ala Tyr Trp Val Met Leu Met Met Met Val Cys Ile Thr  
 1 5 10 15  
 Ala Pro Leu Pro Glu Gly Gly Lys Pro Asn Ser Gly Ile Arg Gly Leu  
 20 25 30  
 Val Pro Asn Asp Leu Thr Pro Gln His Thr Leu Arg Ser Leu Ile Ser  
 35 40 45  
 Arg Arg Gln Thr Asp Val Leu Leu Asp Ala Thr Leu Leu Thr Thr Pro  
 50 55 60  
 Ala Pro Glu Gln Arg Leu Phe Cys Phe Trp Lys Ser Cys Trp Pro Arg

65                      70                      75                      80

Pro Tyr Pro Trp Arg Arg Arg Asn Leu Asn Gly Lys Arg  
85 90

<210>	42
<211>	40
<212>	PRT
<213>	Conus magus

```

<220>
<221>  PEPTIDE
<222>  (1)..(40)
<223>  Xaa at residue 1 is Gln or pyro-Glu; Xaa at residues 14, 16, 29,
        31 and 33 may be Pro or hydroxy-Pro; Xaa at residue 17 may be Glu
        or Gla; Xaa at residues 24, 28 and 34 may be Trp (D or L) or bro
        mo-Trp (D or L)

```

```
<220>
<221>  PEPTIDE
<222>  (1)..(40)
<223>  Xaa at residue 32 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Ty
      r, O-sulpho-Tyr or O-phospho-Tyr
```

<400> 42  
Xaa Thr Asp Val Leu Leu Asp Ala Thr Leu Leu Thr Thr Xaa Ala Xaa  
1 5 10 15

Xaa Gln Arg Leu Phe Cys Phe Xaa Lys Ser Cys Xaa Xaa Arg Xaa Xaa  
20 25 30

Xaa Xaa Arg Arg Arg Asn Leu Asn  
35 40

```
<210> 43
<211> 423
<212> DNA
<213> Conus emaciatus
```

```
<220>
<221> CDS
<222> (1) .. (249)
```

```
<400> 43
atg cag acg gcc tac tgg gtg atg gcg atg atg atg gtg tgg att aca      48
Met Gln Thr Ala Tyr Trp Val Met Ala Met Met Met Val Trp Ile Thr
1          5          10          15
```

gcc cct ctg tct gaa ggt ggt aaa ttg aac gac gta att cgg ggt ttg 96  
Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu  
20 25 30

gtg cca gat gac tta acc cca cag ctt gtt ttg caa agt ctg gat tcc 144  
Val Pro Asp Asp Leu Thr Pro Gln Leu Val Leu Gln Ser Leu Asp Ser  
35 40 45

cgt cgt cat act cac ggc att cgt ccg aag gga gac ggc ata tgt atc 192  
Arg Arg His Thr His Gly Ile Arg Pro Lys Gly Asp Gly Ile Cys Ile  
50 55 60

tgg aag gta tgt cca cca gac cca tgg aga cga cat cgt ctt aag aaa 240  
 Trp Lys Val Cys Pro Pro Asp Pro Trp Arg Arg His Arg Leu Lys Lys  
 65 70 75 80

aga aac aat tgacgtcaga caaccgccac aacttgagta cgacatcgtt 289  
 Arg Asn Asn

aatacgactt cagcaaatat gaaattttca gcatcactgt ggttgtcaag aaatcagttg 349

otttaaaaga ttggatttgt ccttgtttaa gagttgtact gatgtcagct ctgccctgtg 409

aaataaagct gatg 423

<210> 44

<211> 83

<212> PRT

<213> Conus emaciatus

<400> 44

Met Gln Thr Ala Tyr Trp Val Met Ala Met Met Met Val Trp Ile Thr  
 1 5 10 15

Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu  
 20 25 30

Val Pro Asp Asp Leu Thr Pro Gln Leu Val Leu Gln Ser Leu Asp Ser  
 35 40 45

Arg Arg His Thr His Gly Ile Arg Pro Lys Gly Asp Gly Ile Cys Ile  
 50 55 60

Trp Lys Val Cys Pro Pro Asp Pro Trp Arg Arg His Arg Leu Lys Lys  
 65 70 75 80

Arg Asn Asn

<210> 45

<211> 33

<212> PRT

<213> Conus emaciatus

<220>

<221> PEPTIDE

<222> (1)..(33)

<223> Xaa at residues 7, 19, 20 and 22 may be Pro or hydroxy-Pro; Xaa at residues 15 and 23 may be Trp (D or L) or bromo-Trp (D or L)

<400> 45

His Thr His Gly Ile Arg Xaa Lys Gly Asp Gly Ile Cys Ile Xaa Lys  
 1 5 10 15

Val Cys Xaa Xaa Asp Xaa Xaa Arg Arg His Arg Leu Lys Lys Arg Asn  
 20 25 30

Asn

<210> 46

<211> 412

<212> DNA

<213> *Conus circumciscus*

<220>

<221> CDS

<222> (1)..(240)

<400> 46

atg	cag	acg	gcc	tac	tgg	gtg	atg	gtg	atg	atg	gtg	gtg	tgg	att	aca	48
Met	Gln	Thr	Ala	Tyr	Trp	Val	Met	Val	Met	Met	Val	Val	Trp	Ile	Thr	
1				5				10						15		

gcc	cct	ctg	tct	gaa	ggg	ggg	aaa	tcg	aac	gac	gta	att	cgg	ggg	ttg	96
Ala	Pro	Leu	Ser	Glu	Gly	Gly	Lys	Ser	Asn	Asp	Val	Ile	Arg	Gly	Leu	
			20					25					30			

gtg	cca	cac	atc	tta	acc	cca	cag	cat	atc	ttg	caa	agt	ctg	act	tcc	144
Val	Pro	His	Ile	Leu	Thr	Pro	Gln	His	Ile	Leu	Gln	Ser	Leu	Thr	Ser	
		35					40					45				

cgt	ctt	cgt	tct	gac	agc	agt	ggg	cag	aaa	gga	gca	caa	ata	tgc	atc	192
Arg	Leu	Arg	Ser	Asp	Ser	Ser	Gly	Gln	Lys	Gly	Ala	Gln	Ile	Cys	Ile	
	50					55					60					

tgg	aag	gta	tgt	cca	cta	tcc	cca	tgg	aga	cga	cca	caa	gga	aaa	aga	240
Trp	Lys	Val	Cys	Pro	Leu	Ser	Pro	Trp	Arg	Arg	Pro	Gln	Gly	Lys	Arg	
65					70				75					80		

tgaatgacgt	cagacaaccg	ctacaactgt	agtacgacat	cgttgatacg	acttcagcaa	300
------------	------------	------------	------------	------------	------------	-----

atattttaaac	atcactgtgg	ttgtgaagaa	atcagttgct	ttaaaagatt	ggattttttcc	360
-------------	------------	------------	------------	------------	-------------	-----

ttgtttaaga	gttgtactga	tatcagctct	gccctgtgaa	ataaagctga	tg	412
------------	------------	------------	------------	------------	----	-----

<210> 47

<211> 80

<212> PRT

<213> *Conus circumciscus*

<400> 47

Met	Gln	Thr	Ala	Tyr	Trp	Val	Met	Val	Met	Met	Val	Val	Trp	Ile	Thr
1				5				10						15	

Ala	Pro	Leu	Ser	Glu	Gly	Gly	Lys	Ser	Asn	Asp	Val	Ile	Arg	Gly	Leu
			20					25					30		

Val	Pro	His	Ile	Leu	Thr	Pro	Gln	His	Ile	Leu	Gln	Ser	Leu	Thr	Ser
		35					40					45			

Arg	Leu	Arg	Ser	Asp	Ser	Ser	Gly	Gln	Lys	Gly	Ala	Gln	Ile	Cys	Ile
	50					55					60				

Trp	Lys	Val	Cys	Pro	Leu	Ser	Pro	Trp	Arg	Arg	Pro	Gln	Gly	Lys	Arg
65					70				75					80	

<210> 48

<211> 28

<212> PRT

<213> *Conus circumciscus*

<220>

<221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residues 16 and 24 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 20, 23 and 27 may be Pro or hydroxy-Pro  
  
 <400> 48  
 Leu Arg Ser Asp Ser Ser Gly Gln Lys Gly Ala Gln Ile Cys Ile Xaa  
 1 5 10 15  
 Lys Val Cys Xaa Leu Ser Xaa Xaa Arg Arg Xaa Gln  
 20 25  
  
 <210> 49  
 <211> 410  
 <212> DNA  
 <213> Conus betulinus  
  
 <220>  
 <221> CDS  
 <222> (1)..(207)  
  
 <400> 49  
 atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15  
 gcc cct ctg tcc gaa ggt ggt aaa ctg aac gat gta att cgg gct ttg 96  
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Ala Leu  
 20 25 30  
  
 gcg cca gac gac gta acc cca cag ttt atc ttg cga agt ctg att tcc 144  
 Ala Pro Asp Asp Val Thr Pro Gln Phe Ile Leu Arg Ser Leu Ile Ser  
 35 40 45  
  
 cgt cgt cgt tct gac agc gat gtt cgg gag gta ccc gta tgt tcc tgg 192  
 Arg Arg Arg Ser Asp Ser Asp Val Arg Glu Val Pro Val Cys Ser Trp  
 50 55 60  
  
 aag ata tgt cca cca tagccataga gacgacatga tottaaggaa aaagagaaat 247  
 Lys Ile Cys Pro Pro  
 65  
  
 gacgtcagac aaccgccaca actgtagtac ggcacgtta atacgacttc agcaaattgtt 307  
 ttaacatcac tgtggttgtg aagaaatcag ctgctttaaa agattggatt tttccttaag 367  
 agttgcactg atgtcagttc tgccctgtga aataaagctg atg 410  
  
 <210> 50  
 <211> 69  
 <212> PRT  
 <213> Conus betulinus  
  
 <400> 50  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15  
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Ala Leu  
 20 25 30  
 Ala Pro Asp Asp Val Thr Pro Gln Phe Ile Leu Arg Ser Leu Ile Ser

35 40 45  
 Arg Arg Arg Ser Asp Ser Asp Val Arg Glu Val Pro Val Cys Ser Trp  
 50 55 60

Lys Ile Cys Pro Pro  
 65

<210> 51  
 <211> 19  
 <212> PRT  
 <213> Conus betulinus

<220>  
 <221> PEPTIDE  
 <222> (1)..(19)  
 <223> Xaa at residue 8 may be Glu or Gla; Xaa at residues 10, 18 and 19  
 may be Pro or hydroxy-Pro; Xaa at residue 14 may be Trp (D or L)  
 or bromo-Trp (D or L)

<400> 51  
 Arg Ser Asp Ser Asp Val Arg Xaa Val Xaa Val Cys Ser Xaa Lys Ile  
 1 5 10 15

Cys Xaa Xaa

<210> 52  
 <211> 423  
 <212> DNA  
 <213> Conus aurisiacus

<220>  
 <221> CDS  
 <222> (1)..(249)

<400> 52  
 atg cag acg gcc tac tgg gtg atg gcg atg atg atg gtg tgg att aca 48  
 Met Gln Thr Ala Tyr Trp Val Met Ala Met Met Met Val Trp Ile Thr  
 1 5 10 15

gcc cct ctg tct gaa ggt ggt aaa ttg aac gac gta att cgg ggt ttg 96  
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu  
 20 25 30

gtg cca gat gac tta acc cca cag ctt gtt ttg caa agt ctg gat tcc 144  
 Val Pro Asp Asp Leu Thr Pro Gln Leu Val Leu Gln Ser Leu Asp Ser  
 35 40 45

cgt cgt cat act cac ggc att cgt ccg aag gga gac ggc ata tgt atc 192  
 Arg Arg His Thr His Gly Ile Arg Pro Lys Gly Asp Gly Ile Cys Ile  
 50 55 60

tgg aag gta tgt cca cca gac cca tgg aga cga cat cat ctt aag aaa 240  
 Trp Lys Val Cys Pro Pro Asp Pro Trp Arg Arg His His Leu Lys Lys  
 65 70 75 80

aga aac aat tgacgtcaga caaccgccac aacttgagta cgacatcggt 289  
 Arg Asn Asn



## 25

aatacgactt cagcaaatat gaaattttca gcatcactgt ggttgtcaag aaatcagttg 349  
 ctttaaaaga ttggatttgt ccttgtttaa gagttgtact gatgtcagct ctgccctatg 409  
 aaataaagct gatg 423

<210> 53  
 <211> 83  
 <212> PRT  
 <213> Conus aurisiacus

<400> 53  
 Met Gln Thr Ala Tyr Trp Val Met Ala Met Met Val Trp Ile Thr  
 1 5 10 15  
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu  
 20 25 30  
 Val Pro Asp Asp Leu Thr Pro Gln Leu Val Leu Gln Ser Leu Asp Ser  
 35 40 45  
 Arg Arg His Thr His Gly Ile Arg Pro Lys Gly Asp Gly Ile Cys Ile  
 50 55 60  
 Trp Lys Val Cys Pro Pro Asp Pro Trp Arg Arg His His Leu Lys Lys  
 65 70 75 80

Arg Asn Asn

<210> 54  
 <211> 33  
 <212> PRT  
 <213> Conus aurisiacus

<220>  
 <221> PEPTIDE  
 <222> (1)..(33)  
 <223> Xaa at residues 7, 19, 20 and 22 may be Pro or hydroxy-Pro; Xaa at residues 1 and 24 may be Trp (D or L) or bromo-Trp (D or L)

<400> 54  
 His Thr His Gly Ile Arg Xaa Lys Gly Asp Gly Ile Cys Ile Xaa Lys  
 1 5 10 15  
 Val Cys Xaa Xaa Asp Xaa Xaa Arg Arg His His Leu Lys Lys Arg Asn  
 20 25 30

Asn

<210> 55  
 <211> 439  
 <212> DNA  
 <213> Conus aurisiacus

<220>  
 <221> CDS  
 <222> (1)..(249)

<400> 55

atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15

gcc cct ctg tct gaa ggt ggt aaa ttg aac gac gta att tgg ggt ttg 96  
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Trp Gly Leu  
 20 25 30

gtg cca cac atc tta acc cca cag cat atc ttg caa agc ctg act tcc 144  
 Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Leu Thr Ser  
 35 40 45

cgt ctt cat tct gac agc agt gat cag aaa gga ggc atg aac gca tgg 192  
 Arg Leu His Ser Asp Ser Ser Asp Gln Lys Gly Gly Met Asn Ala Trp  
 50 55 60

aca gga gca gga gca caa ata tgc atc tgg aag gta tgt cca cca ccc 240  
 Thr Gly Ala Gly Ala Gln Ile Cys Ile Trp Lys Val Cys Pro Pro Pro  
 65 70 75 80

cca tgg aga tgaacacaag gaaaaagatg aatgacgtca gacaaccgcc 289  
 Pro Trp Arg

acaactgtag tacgacatcg ttgatacgac ttcagcaaat attttaacat cactgtggtt 349

gtgaagaaat cagttgcttt aaaagattgg atttttcctt gtttaagagt tgtactgata 409

tcagctctgc cctgtgaagt aaagctgatg 439

<210> 56

<211> 83

<212> PRT

<213> Conus aurisiacus

<400> 56

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15

Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Trp Gly Leu  
 20 25 30

Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Leu Thr Ser  
 35 40 45

Arg Leu His Ser Asp Ser Ser Asp Gln Lys Gly Gly Met Asn Ala Trp  
 50 55 60

Thr Gly Ala Gly Ala Gln Ile Cys Ile Trp Lys Val Cys Pro Pro Pro  
 65 70 75 80

Pro Trp Arg

<210> 57

<211> 34

<212> PRT

<213> Conus aurisiacus

<220>

<221> PEPTIDE  
 <222> (1)..(34)  
 <223> Xaa at residues 15, 25 and 33 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 29, 30, 31 and 32 may be Pro or hydroxy-Pro

<400> 57  
 Leu His Ser Asp Ser Ser Asp Gln Lys Gly Gly Met Asn Ala Xaa Thr  
 1 5 10 15  
 Gly Ala Gly Ala Gln Ile Cys Ile Xaa Lys Val Cys Xaa Xaa Xaa Xaa  
 20 25 30

Xaa Arg

<210> 58  
 <211> 412  
 <212> DNA  
 <213> Conus aurisiacus

<220>  
 <221> CDS  
 <222> (1)..(222)

<400> 58  
 atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15  
 gcc cct ctg tct gaa ggt ggt aaa ttg aac gac gta att tgg ggt ttg 96  
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Trp Gly Leu  
 20 25 30  
 gtg cca cac atc tta acc cca cag cat atc ttg caa agc ctg act tcc 144  
 Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Leu Thr Ser  
 35 40 45  
 cgt ctt cat tct gac agc agt gat cag aaa gga gca caa ata tgc atc 192  
 Arg Leu His Ser Asp Ser Ser Asp Gln Lys Gly Ala Gln Ile Cys Ile  
 50 55 60  
 tgg aag gta tgt cca cca ccc cca tgg aga tgaacacaag gaaaaagatg 242  
 Trp Lys Val Cys Pro Pro Pro Pro Trp Arg  
 65 70  
 aatgacgtca gacaaccgcc acaactgtag tacgacatcg ttgatacgac ttcagcaaat 302  
 attttaacat cactgtgggt gtgaagaaat cagttgcttt aaaagattgg atttttcctt 362  
 gtttaggagt tgtattgata tcagctctgc cctgtgaaat aaagctgatg 412

<210> 59  
 <211> 74  
 <212> PRT  
 <213> Conus aurisiacus

<400> 59  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15

Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Trp Gly Leu  
                   20                  25                  30

Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Leu Thr Ser  
           35                  40                  45

Arg Leu His Ser Asp Ser Ser Asp Gln Lys Gly Ala Gln Ile Cys Ile  
       50                  55                  60

Trp Lys Val Cys Pro Pro Pro Pro Trp Arg  
       65                  70

<210> 60

<211> 25

<212> PRT

<213> Conus aurisiacus

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residues 16 and 24 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 20, 21, 22 and 23 may be Pro or hydroxy-Pro

<400> 60

Leu His Ser Asp Ser Ser Asp Gln Lys Gly Ala Gln Ile Cys Ile Xaa  
   1                  5                  10                  15

Lys Val Cys Xaa Xaa Xaa Xaa Xaa Arg  
           20                  25

<210> 61

<211> 439

<212> DNA

<213> Conus aurisiacus

<220>

<221> CDS

<222> (1)..(267)

<400> 61

atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca           48  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
   1                  5                  10                  15

gcc cct ctg ttt gaa ggt ggt aaa ttg aac gac gta att cgg ggt ttg           96  
 Ala Pro Leu Phe Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu  
           20                  25                  30

gtg cca cac atc tta acc cca cag cat atc ttg caa agc ctg act tcc           144  
 Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Leu Thr Ser  
           35                  40                  45

cgt ctt cgt tct gac agc agt gat cag aaa gga ggc atg aac gca tcg           192  
 Arg Leu Arg Ser Asp Ser Ser Asp Gln Lys Gly Gly Met Asn Ala Ser  
       50                  55                  60

aca gga gca gga gca caa ata tgc atc tgg aag gta tgt cca cca tcc           240  
 Thr Gly Ala Gly Ala Gln Ile Cys Ile Trp Lys Val Cys Pro Pro Ser  
       65                  70                  75                  80

cca tgg aga cga aca caa gga aaa aga tgaatgacgt cagacaaccg 287  
 Pro Trp Arg Arg Thr Gln Gly Lys Arg  
 85

ccacaactgt agtacgacat cgttgatacg acttcagcaa atattttaac atcactgtgg 347

ttgtgaagaa atcagttgct ttaaaagatt ggatttttcc ttgtttaaga gttgtactga 407

tatcagctct gcactgtgaa ataaagctga tg 439

<210> 62

<211> 89

<212> PRT

<213> Conus aurisiacus

<400> 62

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15

Ala Pro Leu Phe Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu  
 20 25 30

Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Leu Thr Ser  
 35 40 45

Arg Leu Arg Ser Asp Ser Ser Asp Gln Lys Gly Gly Met Asn Ala Ser  
 50 55 60

Thr Gly Ala Gly Ala Gln Ile Cys Ile Trp Lys Val Cys Pro Pro Ser  
 65 70 75 80

Pro Trp Arg Arg Thr Gln Gly Lys Arg  
 85

<210> 63

<211> 37

<212> PRT

<213> Conus aurisiacus

<220>

<221> PEPTIDE

<222> (1)..(37)

<223> Xaa at residues 25 and 33 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 29, 30 and 32 may be Pro or hydroxy-Pro

<400> 63

Leu Arg Ser Asp Ser Ser Asp Gln Lys Gly Gly Met Asn Ala Ser Thr  
 1 5 10 15

Gly Ala Gly Ala Gln Ile Cys Ile Xaa Lys Val Cys Xaa Xaa Ser Xaa  
 20 25 30

Xaa Arg Arg Thr Gln  
 35

<210> 64

<211> 412

<212> DNA

<213> Conus achatinus

<220>  
 <221> CDS  
 <222> (1)..(240)

<400> 64  
 atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15  
 gcc cct ctg tct gaa ggt ggt aaa ttg aac gac gta att cgg ggt ttg 96  
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu  
 20 25 30  
 gtg cca cac atc tta acc cca cag cat atc ttg caa agt ctg act tcc 144  
 Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Leu Thr Ser  
 35 40 45  
 cgt ctt cgt tct gac aac ggt ggt tcg agt gga gca caa ata tgc atc 192  
 Arg Leu Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile  
 50 55 60  
 tgg aag gtg tgt cca cca tcc cca tgg aga cga cca caa gga aaa aga 240  
 Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Arg Pro Gln Gly Lys Arg  
 65 70 75 80  
 tgaacggcgt cagacaaccg ccacaactgt agtgggacat cgttgatacg acttcagcaa 300  
 atattttaac atcactgtgg ttgtgaagaa atcagttgct ttaaaagatt ggatttttcc 360  
 ttgtttaaga gttgtactga tatcagctct gccctatgaa ataaagctga tg 412

<210> 65  
 <211> 80  
 <212> PRT  
 <213> Conus achatinus

<400> 65  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15  
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu  
 20 25 30  
 Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Leu Thr Ser  
 35 40 45  
 Arg Leu Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile  
 50 55 60  
 Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Arg Pro Gln Gly Lys Arg  
 65 70 75 80

<210> 66  
 <211> 28  
 <212> PRT  
 <213> Conus achatinus

<220>  
 <221> PEPTIDE  
 <222> (1)..(28)

<223> Xaa at residues 16 and 24 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 20, 21, 23 and 27 may be Pro or hydroxy-Pro

<400> 66

Leu Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile Xaa  
1 5 10 15

Lys Val Cys Xaa Xaa Ser Xaa Xaa Arg Arg Xaa Gln  
20 25

<210> 67

<211> 399

<212> DNA

<213> *Conus purpurascens*

<220>

<221> CDS

<222> (1)..(213)

<400> 67

atg cag acg gcc tac tgg gtg atg gtg atg acg atg gtg tgg att aca 48  
Met Gln Thr Ala Tyr Trp Val Met Val Met Thr Met Val Trp Ile Thr  
1 5 10 15

gcc cct ctg tct gaa ggt gga aaa ctg aac gat gta att cgg ggt ttg 96  
Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu  
20 25 30

gtg cca gac gac tta gcc cta cag ctt atc ttg caa agt ccg gtt ttc 144  
Val Pro Asp Asp Leu Ala Leu Gln Leu Ile Leu Gln Ser Pro Val Phe  
35 40 45

cgt cgt caa tct gaa gag gaa aaa ata tgc ctc tgg aag ata tgt cca 192  
Arg Arg Gln Ser Glu Glu Glu Lys Ile Cys Leu Trp Lys Ile Cys Pro  
50 55 60

cca ccc cca tgg aga cga tca taaggaaaaaaa aaaatgaatg acgtcagaca 243  
Pro Pro Pro Trp Arg Arg Ser  
65 70

accaccacaa ctgtaatacgc acatcgttaa tacgacttca gcaaacattt taacatcact 303

gtgggttgga agaaatcagt tgctttagaa gcttggattt ttccttggtt aagagttgta 363

ctgatatcag ctctgcccta tgaaataaag ctgatg 399

<210> 68

<211> 71

<212> PRT

<213> *Conus purpurascens*

<400> 68

Met Gln Thr Ala Tyr Trp Val Met Val Met Thr Met Val Trp Ile Thr  
1 5 10 15

Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu  
20 25 30

Val Pro Asp Asp Leu Ala Leu Gln Leu Ile Leu Gln Ser Pro Val Phe  
35 40 45

Arg Arg Gln Ser Glu Glu Glu Lys Ile Cys Leu Trp Lys Ile Cys Pro  
 50 55 60

Pro Pro Pro Trp Arg Arg Ser  
 65 70

<210> 69  
 <211> 21  
 <212> PRT  
 <213> Conus purpurascens

<220>  
 <221> PEPTIDE  
 <222> (1)..(21)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residues 3,4 and 5 may be Glu or Ala; Xaa at residues 10 and 18 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 14, 15, 16 and 17 may be Pro or hydroxy-Pro

<400> 69  
 Xaa Ser Xaa Xaa Xaa Lys Ile Cys Leu Xaa Lys Ile Cys Xaa Xaa Xaa  
 1 5 10 15

Xaa Xaa Arg Arg Ser  
 20

<210> 70  
 <211> 398  
 <212> DNA  
 <213> Conus purpurascens

<220>  
 <221> CDS  
 <222> (1)..(213)

<400> 70  
 atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15

gcc cct ctg tct gag ggt aga aaa ccg aac gat gta att cgg ggt ttg 96  
 Ala Pro Leu Ser Glu Gly Arg Lys Pro Asn Asp Val Ile Arg Gly Leu  
 20 25 30

gtg cca gat gac tta gcc cta cag ctt atc ttg caa agt cag gtt tcc 144  
 Val Pro Asp Asp Leu Ala Leu Gln Leu Ile Leu Gln Ser Gln Val Ser  
 35 40 45

cgt cgt gaa tct aat ggg gtg gaa ata tgc atg tgg aag gta tgt cca 192  
 Arg Arg Glu Ser Asn Gly Val Glu Ile Cys Met Trp Lys Val Cys Pro  
 50 55 60

cca tcc cca tgg aga cga tca taaggaaaaa aaatgaatga cgtcagacaa 243  
 Pro Ser Pro Trp Arg Arg Ser  
 65 70

ccaccacaac tgtaatacga catcggttaat acgacttcag caaacatttt aacatcactg 303

tgggtgtgaa gaaatcagtt gctttaaaag attggatttt tccttgttta agagttgtac 363



tgatatcagc tctgccctat gaaataaagc tgatg 398

<210> 71  
 <211> 71  
 <212> PRT  
 <213> Conus purpurascens

<400> 71  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15  
 Ala Pro Leu Ser Glu Gly Arg Lys Pro Asn Asp Val Ile Arg Gly Leu  
 20 25 30  
 Val Pro Asp Asp Leu Ala Leu Gln Leu Ile Leu Gln Ser Gln Val Ser  
 35 40 45  
 Arg Arg Glu Ser Asn Gly Val Glu Ile Cys Met Trp Lys Val Cys Pro  
 50 55 60  
 Pro Ser Pro Trp Arg Arg Ser  
 65 70

<210> 72  
 <211> 21  
 <212> PRT  
 <213> Conus purpurascens

<220>  
 <221> PEPTIDE  
 <222> (1)..(21)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 may be Glu  
 or Gla; Xaa at residues 10 and 18 may be Trp (D or L) or bromo-Trp  
 (D or L); Xaa at residues 14, 15 and 17 may be Pro or hydroxy-Pro

<400> 72  
 Xaa Ser Asn Gly Val Xaa Ile Cys Met Xaa Lys Val Cys Xaa Xaa Ser  
 1 5 10 15  
 Xaa Xaa Arg Arg Ser  
 20

<210> 73  
 <211> 409  
 <212> DNA  
 <213> Conus stercusmuscarum

<220>  
 <221> CDS  
 <222> (1)..(213)

<400> 73  
 atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15

gcc cct ctg tct gaa ggt ggt aaa ttg acc gac gta att cgg ggt ttg 96  
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Thr Asp Val Ile Arg Gly Leu

	20	25	30	
gtg cca cac atc tta acc cca cag cat atc ttg caa agt atg act tcc				144
Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Met Thr Ser				
	35	40	45	
cgt ctt ggt att ggc agc agt gat caa aat gca caa ata tgc atc tgg				192
Arg Leu Gly Ile Gly Ser Ser Asp Gln Asn Ala Gln Ile Cys Ile Trp				
	50	55	60	
aag gta tgt cca cca tcc cca tagagacgac cataaggaaa aagatgaatg				243
Lys Val Cys Pro Pro Ser Pro				
	65	70		
acgtcagaca accgccacaa ctgtagtacg acatcggttga tacgacttca gcaaatatatt				303
taacatcact gtgggttgtga agaaatcagt tgctttaaaa gatttgattt ttccttgattt				363
aagagttgta ctgatatcag ctctgccctg tgaaataaag ctgatg				409
<210> 74				
<211> 71				
<212> PRT				
<213> Conus stercusmuscarum				
<400> 74				
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr				
1 5 10 15				
Ala Pro Leu Ser Glu Gly Gly Lys Leu Thr Asp Val Ile Arg Gly Leu				
20 25 30				
Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Met Thr Ser				
35 40 45				
Arg Leu Gly Ile Gly Ser Ser Asp Gln Asn Ala Gln Ile Cys Ile Trp				
50 55 60				
Lys Val Cys Pro Pro Ser Pro				
65 70				
<210> 75				
<211> 22				
<212> PRT				
<213> Conus stercusmuscarum				
<220>				
<221> PEPTIDE				
<222> (1)..(22)				
<223> Xaa at residue 15 may be Trp or bromo-Trp; Xaa at residue 19, 20 and 22 may be Pro or hydroxy-Pro				
<400> 75				
Leu Gly Ile Gly Ser Ser Asp Gln Asn Ala Gln Ile Cys Ile Xaa Lys				
1 5 10 15				
Val Cys Xaa Xaa Ser Xaa				
20				
<210> 76				

<211> 433  
 <212> DNA  
 <213> Conus baileyi

<220>  
 <221> CDS  
 <222> (1)..(216)

<400> 76  
 atg cag acg gcc tac tgg gtg atg gtg atg ata atg gtg tgg att aca 48  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Ile Met Val Trp Ile Thr  
 1 5 10 15  
 gtc cct ctg tct gaa ggt ggt aaa ttg aac gac ata att cgg ggt ttg 96  
 Val Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Ile Ile Arg Gly Leu  
 20 25 30  
 ttg cca gac aac ttc ccc cca cag ctt acc ttg cat cgt ctg gtt tcc 144  
 Leu Pro Asp Asn Phe Pro Pro Gln Leu Thr Leu His Arg Leu Val Ser  
 35 40 45  
 cgt cgt cat tct gac agc att att ctg agg ggc tta tgt atc tgg aag 192  
 Arg Arg His Ser Asp Ser Ile Ile Leu Arg Gly Leu Cys Ile Trp Lys  
 50 55 60  
 gtg tgt gaa cct ccg cca caa aga tgatctgggtc caaagccaaa aaacgaatga 246  
 Val Cys Glu Pro Pro Pro Gln Arg  
 65 70  
 tgtcagacaa ccgccacagc ttagtagcga catggttaat acgacttcag caaatatttc 306  
 aacatcactg tggttgtgaa gaaatcagtt actttaaaaag attggaatga tgtcagctgt 366  
 gcactatcaa ataaagttga tgtgacaaaa aaaaaaaaaa aaaaagtact ctgcgttggt 426  
 actcgag 433

<210> 77  
 <211> 72  
 <212> PRT  
 <213> Conus baileyi

<400> 77  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Ile Met Val Trp Ile Thr  
 1 5 10 15  
 Val Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Ile Ile Arg Gly Leu  
 20 25 30  
 Leu Pro Asp Asn Phe Pro Pro Gln Leu Thr Leu His Arg Leu Val Ser  
 35 40 45  
 Arg Arg His Ser Asp Ser Ile Ile Leu Arg Gly Leu Cys Ile Trp Lys  
 50 55 60  
 Val Cys Glu Pro Pro Pro Gln Arg  
 65 70

<210> 78  
 <211> 22

<212> PRT  
 <213> *Conus baileyi*

<220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa at residue 13 may be Trp (D or L) or bromo-Trp (D or L); Xaa  
 at residue 17 may be Glu or Gla; Xaa at residues 18, 19 and 20 ma  
 y be Pro or hydroxy-Pro

<400> 78  
 His Ser Asp Ser Ile Ile Leu Arg Gly Leu Cys Ile Xaa Lys Val Cys  
 1 5 10 15  
 Xaa Xaa Xaa Xaa Gln Arg  
 20

<210> 79  
 <211> 413  
 <212> DNA  
 <213> *Conus bocki*

<220>  
 <221> CDS  
 <222> (1)..(270)

<400> 79  
 atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15  
 gcc cct ctg tct gaa agt gat aaa ctg aac gac gta att cgg ggt ttg 96  
 Ala Pro Leu Ser Glu Ser Asp Lys Leu Asn Asp Val Ile Arg Gly Leu  
 20 25 30  
 gtg cca gac aac tta acc cca cag ctt atc ttg cga agt ctg att tcc 144  
 Val Pro Asp Asn Leu Thr Pro Gln Leu Ile Leu Arg Ser Leu Ile Ser  
 35 40 45  
 cgt cgt cgt tct gac aag gat gat ccg gga gga caa gaa tgt tac tgg 192  
 Arg Arg Arg Ser Asp Lys Asp Asp Pro Gly Gly Gln Glu Cys Tyr Trp  
 50 55 60  
 aac gta tgt gca cca aac cag gga gac cac atg atc tta aga aaa aag 240  
 Asn Val Cys Ala Pro Asn Gln Gly Asp His Met Ile Leu Arg Lys Lys  
 65 70 75 80  
 atg aat gac gac aga caa ccg cca caa ctg taatacgaca tcgttaatac 290  
 Met Asn Asp Asp Arg Gln Pro Pro Gln Leu  
 85 90  
 gacttcagca aatatttttaa catcactgtg gttgtgaaga aatcagttgc tttaaaagat 350  
 tggattttttc cgtgttttaag agctgtactg atatctgctc tgccctgtga aataaagctg 410  
 atg 413

<210> 80  
 <211> 90  
 <212> PRT  
 <213> *Conus bocki*

&lt;400&gt; 80

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15

Ala Pro Leu Ser Glu Ser Asp Lys Leu Asn Asp Val Ile Arg Gly Leu  
 20 25 30

Val Pro Asp Asn Leu Thr Pro Gln Leu Ile Leu Arg Ser Leu Ile Ser  
 35 40 45

Arg Arg Arg Ser Asp Lys Asp Asp Pro Gly Gly Gln Glu Cys Tyr Trp  
 50 55 60

Asn Val Cys Ala Pro Asn Gln Gly Asp His Met Ile Leu Arg Lys Lys  
 65 70 75 80

Met Asn Asp Asp Arg Gln Pro Pro Gln Leu  
 85 90

&lt;210&gt; 81

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Conus bocki

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(40)

<223> Xaa at residues 7, 19, 37, 38 may be Pro or hydroxy-Pro; Xaa at r  
 esidue 11 may be Glu or Gla; Xaa at residue 14 may be Trp (D or L  
 ) or bromo-Trp (D or L); Xaa at residue 13 may be Tyr, 125I-Tyr,  
 mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

&lt;400&gt; 81

Arg Ser Asp Lys Asp Asp Xaa Gly Gly Gln Xaa Cys Xaa Xaa Asn Val  
 1 5 10 15

Cys Ala Xaa Asn Gln Gly Asp His Met Ile Leu Arg Lys Lys Met Asn  
 20 25 30

Asp Asp Arg Gln Xaa Xaa Gln Leu  
 35 40

&lt;210&gt; 82

&lt;211&gt; 496

&lt;212&gt; DNA

&lt;213&gt; Conus chaldaeus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (21)..(260)

&lt;400&gt; 82

gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg atg ggg atg 53  
 Met Gln Thr Ala Tyr Trp Val Met Met Gly Met  
 1 5 10

atg atg gtg tgg att aca gcc cct ctg tct gga ggt ggt aaa ctg aac 101  
 Met Met Val Trp Ile Thr Ala Pro Leu Ser Gly Gly Gly Lys Leu Asn  
 15 20 25

gac gta att cgg ggt ttg gtg cca gac gac tta acc cta cag cgt atg 149  
 Asp Val Ile Arg Gly Leu Val Pro Asp Asp Leu Thr Leu Gln Arg Met  
 30 35 40

ttc gaa act ccg gtt tcc cat cgt ctt tct gag ggc aga aat tcg acg 197  
 Phe Glu Thr Pro Val Ser His Arg Leu Ser Glu Gly Arg Asn Ser Thr  
 45 50 55

gta cac ata tgt acg tgg aag gta tgt cca cct ccc cca tgg aga cga 245  
 Val His Ile Cys Thr Trp Lys Val Cys Pro Pro Pro Pro Trp Arg Arg  
 60 65 70 75

cca cat gga caa aga tgaatgacgt cagacaacct ccacaactgt agtacgacat 300  
 Pro His Gly Gln Arg  
 80

cgtaaacacg acgtcagcta atcttttaac atcactgtgg ctgtgaagaa ctcggttgct 360

ttaaaagatt ggatttttcc ttgtttaaga gttgtgctga tatgaactct gcactacgaa 420

ataaagctga tgtgacaaac aaaaaaaaga aaaaaaaaag tactctgcgt tgttactcga 480

gcttaagggc gaattc 496

<210> 83  
 <211> 80  
 <212> PRT  
 <213> Conus chaldaeus

<400> 83  
 Met Gln Thr Ala Tyr Trp Val Met Met Gly Met Met Met Val Trp Ile  
 1 5 10 15  
 Thr Ala Pro Leu Ser Gly Gly Gly Lys Leu Asn Asp Val Ile Arg Gly  
 20 25 30  
 Leu Val Pro Asp Asp Leu Thr Leu Gln Arg Met Phe Glu Thr Pro Val  
 35 40 45  
 Ser His Arg Leu Ser Glu Gly Arg Asn Ser Thr Val His Ile Cys Thr  
 50 55 60  
 Trp Lys Val Cys Pro Pro Pro Pro Trp Arg Arg Pro His Gly Gln Arg  
 65 70 75 80

<210> 84  
 <211> 29  
 <212> PRT  
 <213> Conus chaldaeus

<220>  
 <221> PEPTIDE  
 <222> (1)..(29)  
 <223> Xaa at residue 3 may be Glu or Gla; Xaa at residues 14 and 22 may  
 be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 18, 19, 2  
 0, 21 and 25 may be Pro or hydroxy-Pro

<400> 84  
 Leu Ser Xaa Gly Arg Asn Ser Thr Val His Ile Cys Thr Xaa Lys Val  
 1 5 10 15

Cys Xaa Xaa Xaa Xaa Xaa Arg Arg Xaa His Gly Gln Arg  
20 25

```
<210> 85
<211> 499
<212> DNA
<213> Conus chaldaeus
```

```
<220>
<221> CDS
<222> (21)..(260)
```

[illegible]

```
<210> 86
<211> 80
<212> PRT
<213> Conus chaldaeus
```

```

<400>      86
Met  Gln  Thr  Ala  Tyr  Trp  Val  Met  Met  Gly  Met  Met  Met  Val  Trp  Ile
1                               5          10          15

Thr  Ala  Pro  Leu  Ser  Gly  Gly  Gly  Lys  Leu  Asn  Asp  Val  Ile  Arg  Gly
                20                25                30

Leu  Val  Pro  Asp  Asp  Leu  Thr  Leu  Gln  Arg  Met  Phe  Glu  Thr  Pro  Val
                35                40                45

```

Ser His Arg Leu Ser Glu Gly Arg Asn Ser Thr Val His Ile Cys Met  
50 55 60

Trp Lys Val Cys Pro Pro Pro Pro Trp Arg Arg Pro His Gly Gln Arg  
65 70 75 80

<210> 87

<211> 29

<212> PRT

<213> *Conus chaldaeus*

<220>

<221> PEPTIDE

<222> (1)..(29)

<223> Xaa at residue 3 may be Glu or Gla; Xaa at residues 14 and 22 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 18, 19, 20, 21 and 25 may be Pro or hydroxy-Pro

<400> 87

Leu Ser Xaa Gly Arg Asn Ser Thr Val His Ile Cys Met Xaa Lys Val  
1 5 10 15

Cys Xaa Xaa Xaa Xaa Xaa Arg Arg Xaa His Gly Gln Arg  
20 25

<210> 88

<211> 490

<212> DNA

<213> *Conus cinereus*

<220>

<221> CDS

<222> (21)..(305)

<400> 88

gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53  
Met Gln Thr Ala Tyr Trp Val Met Val Met Met  
1 5 10

ttg gtg tgg att aca gcc cct ctg cct gag ggt ggt aaa ccg aag cac 101  
Leu Val Trp Ile Thr Ala Pro Leu Pro Glu Gly Gly Lys Pro Lys His  
15 20 25

gta att cgg ggt ttg gta cca gac gac tta acc cca cag cat atc ttg 149  
Val Ile Arg Gly Leu Val Pro Asp Asp Leu Thr Pro Gln His Ile Leu  
30 35 40

cga agt ttg att tcc cgt cgt tca tct ggc tgc agt gtt tcg ttg ggc 197  
Arg Ser Leu Ile Ser Arg Arg Ser Ser Gly Cys Ser Val Ser Leu Gly  
45 50 55

ttc aaa tgc ttc tgg aag agc tgt aca gta atc cca gtg aga cca ttt 245  
Phe Lys Cys Phe Trp Lys Ser Cys Thr Val Ile Pro Val Arg Pro Phe  
60 65 70 75

gta tct ctg gaa gaa gaa aat gaa tgc cag aaa gtc caa ata agt gca 293  
Val Ser Leu Glu Glu Glu Asn Glu Cys Gln Lys Val Gln Ile Ser Ala  
80 85 90

gta tgg ggt cct tgatagcact tcagcaagga tcaactgtggt tgtgaagaaa 345  
Val Trp Gly Pro



95

tcagttgctt taaaagattt gatttttcct tgtttaagag ttgtactgat atcagctctg 405  
 tactatgaaa taaagctgat gtgacaaaca aaaaaaaaaa aaaaaaaagt actctgcgtt 465  
 gttactcgag cttaagggcg aattc 490

<210> 89  
 <211> 95  
 <212> PRT  
 <213> Conus cinereus

<400> 89  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Leu Val Trp Ile Thr  
 1 5 10 15  
 Ala Pro Leu Pro Glu Gly Gly Lys Pro Lys His Val Ile Arg Gly Leu  
 20 25 30  
 Val Pro Asp Asp Leu Thr Pro Gln His Ile Leu Arg Ser Leu Ile Ser  
 35 40 45  
 Arg Arg Ser Ser Gly Cys Ser Val Ser Leu Gly Phe Lys Cys Phe Trp  
 50 55 60  
 Lys Ser Cys Thr Val Ile Pro Val Arg Pro Phe Val Ser Leu Glu Glu  
 65 70 75 80  
 Glu Asn Glu Cys Gln Lys Val Gln Ile Ser Ala Val Trp Gly Pro  
 85 90 95

<210> 90  
 <211> 45  
 <212> PRT  
 <213> Conus cinereus

<220>  
 <221> PEPTIDE  
 <222> (1)..(45)  
 <223> Xaa at residues 14 and 43 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 21, 24 and 45 may be Pro or hydroxy-Pro; Xaa at residues 29, 30, 31 and 33 may be Glu or Glu

<400> 90  
 Ser Ser Gly Cys Ser Val Ser Leu Gly Phe Lys Cys Phe Xaa Lys Ser  
 1 5 10 15  
 Cys Thr Val Ile Xaa Val Arg Xaa Phe Val Ser Leu Xaa Xaa Xaa Asn  
 20 25 30  
 Xaa Cys Gln Lys Val Gln Ile Ser Ala Val Xaa Gly Xaa  
 35 40 45

<210> 91  
 <211> 497  
 <212> DNA  
 <213> Conus cinereus

<220>  
 <221> CDS

<222> (21)..(263)

<400> 91

gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53  
Met Gln Thr Ala Tyr Trp Val Met Val Met Met  
1 5 10

gtg gtg gtg tgg att aca gcc cct ctg cct gaa ggt ggt aaa ccg gag 101  
Val Val Val Trp Ile Thr Ala Pro Leu Pro Glu Gly Gly Lys Pro Glu  
15 20 25

cac gta att cgg ggt ttg gtg cca gac gac tta acc cca cag ctt atc 149  
His Val Ile Arg Gly Leu Val Pro Asp Asp Leu Thr Pro Gln Leu Ile  
30 35 40

ttg cga agt ctg att tcc cgt cgt agt tct gac ggc aag gca aaa aga 197  
Leu Arg Ser Leu Ile Ser Arg Arg Ser Ser Asp Gly Lys Ala Lys Arg  
45 50 55

aat tgt ttc tgg aag gca tgt gta cca gaa caa tgg aga caa cgt gat 245  
Asn Cys Phe Trp Lys Ala Cys Val Pro Glu Gln Trp Arg Gln Arg Asp  
60 65 70 75

ctt aag gaa aaa gat gaa tgatgtcaga caaccgccat cactgtagta 293  
Leu Lys Glu Lys Asp Glu  
80

tgacatcggtt aatacgactt aagcaaatat tttaacatca ctgtggatct gaagaaatca 353

gttgcttttaa aagattggat ttttctctgt ttaagagttg tactgatgtc agctctgcac 413

tgtgaaataa agctgatgtg acaaacgaaa aaaaaaaaaa aaaaaaagta ctctgcgttg 473

ttactcgagc ttaagggcga attc 497

<210> 92

<211> 81

<212> PRT

<213> Conus cinereus

<400> 92

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Val Val Val Trp Ile  
1 5 10 15

Thr Ala Pro Leu Pro Glu Gly Gly Lys Pro Glu His Val Ile Arg Gly  
20 25 30

Leu Val Pro Asp Asp Leu Thr Pro Gln Leu Ile Leu Arg Ser Leu Ile  
35 40 45

Ser Arg Arg Ser Ser Asp Gly Lys Ala Lys Arg Asn Cys Phe Trp Lys  
50 55 60

Ala Cys Val Pro Glu Gln Trp Arg Gln Arg Asp Leu Lys Glu Lys Asp  
65 70 75 80

Glu

<210> 93

<211> 30  
 <212> PRT  
 <213> Conus cinereus

<220>  
 <221> PEPTIDE  
 <222> (1)..(30)  
 <223> Xaa at residues 12 and 20 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residue 17 may be Pro or hydroxy-Pro; Xaa at residues 18, 27 and 30 may be Glu or Gla

<400> 93  
 Ser Ser Asp Gly Lys Ala Lys Arg Asn Cys Phe Xaa Lys Ala Cys Val  
 1 5 10 15

Xaa Xaa Gln Xaa Arg Gln Arg Asp Leu Lys Xaa Lys Asp Xaa  
 20 25 30

<210> 94  
 <211> 496  
 <212> DNA  
 <213> Conus cinereus

<220>  
 <221> CDS  
 <222> (21)..(263)

<400> 94  
 gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met  
 1 5 10

atg gtg gtg tgg att aca gcc cct ctg cct gaa ggt ggt aaa ccg aag 101  
 Met Val Val Trp Ile Thr Ala Pro Leu Pro Glu Gly Gly Lys Pro Lys  
 15 20 25

cac gta att cgg ggt ttg gtg cca gac gac tta acc cca cag ctt atc 149  
 His Val Ile Arg Gly Leu Val Pro Asp Asp Leu Thr Pro Gln Leu Ile  
 30 35 40

ttg cga agt ctg att tcc cgt cgt agt tct gac ggc aag gca aaa aga 197  
 Leu Arg Ser Leu Ile Ser Arg Arg Ser Ser Asp Gly Lys Ala Lys Arg  
 45 50 55

aat tgt ttc tgg aag gca tgt gta cca gaa caa tgg aga caa cgt gat 245  
 Asn Cys Phe Trp Lys Ala Cys Val Pro Glu Gln Trp Arg Gln Arg Asp  
 60 65 70 75

cct aag gaa aaa gat gaa tgatgtcaga caaccgccat cactgtagta 293  
 Pro Lys Glu Lys Asp Glu  
 80

tgacatcggt aatacgactt aagcaaatat tttaacatca ctgtggatct gaagaaatca 353

gttgctttaa aagattggat ttttcctcgt ttaagagttg tactgatgtc agctctgcac 413

tgtgaaataa agctgacgtg acaagcaaaa aaaaaaaaaa aaaaaagtac tctgcgttgt 473

tactcgagct taagggcgaa ttc 496

<210> 95  
 <211> 81  
 <212> PRT  
 <213> Conus cinereus

<400> 95  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Val Trp Ile  
 1 5 10 15  
 Thr Ala Pro Leu Pro Glu Gly Gly Lys Pro Lys His Val Ile Arg Gly  
 20 25 30  
 Leu Val Pro Asp Asp Leu Thr Pro Gln Leu Ile Leu Arg Ser Leu Ile  
 35 40 45  
 Ser Arg Arg Ser Ser Asp Gly Lys Ala Lys Arg Asn Cys Phe Trp Lys  
 50 55 60  
 Ala Cys Val Pro Glu Gln Trp Arg Gln Arg Asp Pro Lys Glu Lys Asp  
 65 70 75 80

Glu

<210> 96  
 <211> 30  
 <212> PRT  
 <213> Conus cinereus

<220>  
 <221> PEPTIDE  
 <222> (1)..(30)  
 <223> Xaa at residues 12 and 20 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 17 and 25 may be Pro or hydroxy-Pro; Xaa at residues 18, 27 and 30 may be Glu or Gla

<400> 96  
 Ser Ser Asp Gly Lys Ala Lys Arg Asn Cys Phe Xaa Lys Ala Cys Val  
 1 5 10 15

Xaa Xaa Gln Xaa Arg Gln Arg Asp Xaa Lys Xaa Lys Asp Xaa  
 20 25 30

<210> 97  
 <211> 493  
 <212> DNA  
 <213> Conus cinereus

<220>  
 <221> CDS  
 <222> (21)..(260)

<400> 97  
 gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg ata atg 53  
 Met Gln Thr Ala Tyr Trp Val Met Val Ile Met  
 1 5 10  
 atg gtg tgg att aca gcc cct ctg tct gaa ggt ggt aaa ccg aag cac 101  
 Met Val Trp Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Pro Lys His  
 15 20 25  
 gta att cgg ggt ttg gtg cca gtc gac tta acc cca cag ctt atc ttg 149

Val Ile Arg Gly Leu Val Pro Val Asp Leu Thr Pro Gln Leu Ile Leu  
 30 35 40

cga agt ctg att tcc cgt cgt agt tct gac ggc aag gca aaa aaa caa 197  
 Arg Ser Leu Ile Ser Arg Arg Ser Ser Asp Gly Lys Ala Lys Lys Gln  
 45 50 55

tgt gcc tgg aag aca tgt gta cca acc caa tgg aga cga cgt gat ctt 245  
 Cys Ala Trp Lys Thr Cys Val Pro Thr Gln Trp Arg Arg Arg Asp Leu  
 60 65 70 75

aag gaa aaa gat gaa tgatgtcaga caaccgccat cactgtagta tgacatcgtt 300  
 Lys Glu Lys Asp Glu  
 80

aatacgactt aagcaaatat tttaacatca ctgtggttct gaagaaatca gttgctttaa 360

aagattggat ttttccttgt ttaagagttg tactgatatc agctctgcac tgtgaaataa 420

agctgatgtg acaaacaaaa aaaaaaaaaa aaaaaagtac tctgcgttgt tactcgagct 480

taagggcgaa ttc 493

<210> 98  
 <211> 80  
 <212> PRT  
 <213> Conus cinereus

<400> 98  
 Met Gln Thr Ala Tyr Trp Val Met Val Ile Met Met Val Trp Ile Thr  
 1 5 10 15

Ala Pro Leu Ser Glu Gly Gly Lys Pro Lys His Val Ile Arg Gly Leu  
 20 25 30

Val Pro Val Asp Leu Thr Pro Gln Leu Ile Leu Arg Ser Leu Ile Ser  
 35 40 45

Arg Arg Ser Ser Asp Gly Lys Ala Lys Lys Gln Cys Ala Trp Lys Thr  
 50 55 60

Cys Val Pro Thr Gln Trp Arg Arg Arg Asp Leu Lys Glu Lys Asp Glu  
 65 70 75 80

<210> 99  
 <211> 30  
 <212> PRT  
 <213> Conus cinereus

<220>  
 <221> PEPTIDE  
 <222> (1)..(30)  
 <223> Xaa at residues 12 and 20 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residue 17 may be Pro or hydroxy-Pro; Xaa at residues 27 and 30 may be Glu or Gla

<400> 99  
 Ser Ser Asp Gly Lys Ala Lys Lys Gln Cys Ala Xaa Lys Thr Cys Val  
 1 5 10 15

Xaa Thr Gln Xaa Arg Arg Arg Asp Leu Lys Xaa Lys Asp Xaa  
 20 25 30

<210> 100  
 <211> 496  
 <212> DNA  
 <213> Conus circumcissus

<220>  
 <221> CDS  
 <222> (21)..(263)

<400> 100  
 gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met  
 1 5 10

atg gtg tgg att aca gcc cct ctg tct gaa ggt ggt aaa ttg aac gac 101  
 Met Val Trp Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp  
 15 20 25

gta att cgg ggt ttg gtg cca cac atc tta acc cca cag cat atc ttg 149  
 Val Ile Arg Gly Leu Val Pro His Ile Leu Thr Pro Gln His Ile Leu  
 30 35 40

caa ggt ctg act tcc cgt ctt cgt tct gac agc agt ggt cag aaa gga 197  
 Gln Gly Leu Thr Ser Arg Leu Arg Ser Asp Ser Ser Gly Gln Lys Gly  
 45 50 55

gca caa ata tgc atc tgg aag gta tgt cca cta tcc cca tgg aga cga 245  
 Ala Gln Ile Cys Ile Trp Lys Val Cys Pro Leu Ser Pro Trp Arg Arg  
 60 65 70 75

cca caa gga aaa gat gaa tgacgtcaga caaccgctac aactgtagta 293  
 Pro Gln Gly Lys Asp Glu  
 80

cgacatcggtt gatacgactt cagcaaatat ttttaacatca ctgtggttgt gaagaaatca 353

gctgcttttaa aagattggat ttttccttgt ttaagagttg tactgatatc agctctgcac 413

tatgaaataa agctgatgtg acaaacaaaa aaaaaaaaaa aaaaaaagtac tctgcgttgt 473

tactcgagct taagggcgaa ttc 496

<210> 101  
 <211> 81  
 <212> PRT  
 <213> Conus circumcissus

<400> 101  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15

Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu  
 20 25 30

Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Gly Leu Thr Ser  
 35 40 45

Arg Leu Arg Ser Asp Ser Ser Gly Gln Lys Gly Ala Gln Ile Cys Ile  
 50 55 60

Trp Lys Val Cys Pro Leu Ser Pro Trp Arg Arg Pro Gln Gly Lys Asp  
 65 70 75 80

Glu

<210> 102

<211> 32

<212> PRT

<213> Conus circumcissus

<220>

<221> PEPTIDE

<222> (1)..(32)

<223> Xaa at residues 16 and 24 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 20, 23 and 27 may be Pro or hydroxy-Pro; Xaa at residue 32 may be Glu or Gla

<400> 102

Leu Arg Ser Asp Ser Ser Gly Gln Lys Gly Ala Gln Ile Cys Ile Xaa  
 1 5 10 15

Lys Val Cys Xaa Leu Ser Xaa Xaa Arg Arg Xaa Gln Gly Lys Asp Xaa  
 20 25 30

<210> 103

<211> 496

<212> DNA

<213> Conus consors

<220>

<221> CDS

<222> (21)..(242)

<400> 103

gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met.  
 1 5 10

atg gtg tgg att aca gcc cct ctg tct gaa ggt ggt aaa ttg aac gac 101  
 Met Val Trp Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp  
 15 20 25

gta att cgg ggt ttg gtg cca cac ttc tta acc cca cag cat atc ttg 149  
 Val Ile Arg Gly Leu Val Pro His Phe Leu Thr Pro Gln His Ile Leu  
 30 35 40

caa agt ctg act tcc cgt aat ggt tct ggc agc agt aat cag aaa gaa 197  
 Gln Ser Leu Thr Ser Arg Asn Gly Ser Gly Ser Ser Asn Gln Lys Glu  
 45 50 55

gca caa cta tgc atc tgg aag gta tgt cca cca acc cca tgg aga 242  
 Ala Gln Leu Cys Ile Trp Lys Val Cys Pro Pro Thr Pro Trp Arg  
 60 65 70

tgaccacaag gaaaaagatg aacggcgtca gacaaccgcc acaactgtag tgggacatcg 302

ttgatacgac ttcagcaaat attttaacat cactgtgggt gtgaagaaat cagttgtttt 362

aaaagattgg atttttcctt gtttaagagt tgtactgata tcagctctgc actatgaaat 422  
 aaagctgatg tgacaagcaa aaaaaaaaaa aaaaaaagta ctctgcgttg ttactcgagc 482  
 ttaagggcga attc 496

<210> 104  
 <211> 74  
 <212> PRT  
 <213> Conus consors

<400> 104  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Val Trp Ile Thr  
 1 5 10 15  
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu  
 20 25 30  
 Val Pro His Phe Leu Thr Pro Gln His Ile Leu Gln Ser Leu Thr Ser  
 35 40 45  
 Arg Asn Gly Ser Gly Ser Ser Asn Gln Lys Glu Ala Gln Leu Cys Ile  
 50 55 60  
 Trp Lys Val Cys Pro Pro Thr Pro Trp Arg  
 65 70

<210> 105  
 <211> 25  
 <212> PRT  
 <213> Conus consors

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 10 may be Glu or Gla ; Xaa at residues 16 and 24 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 20, 21 and 23 may be Pro or hydroxy-Pro

<400> 105  
 Asn Gly Ser Gly Ser Ser Asn Gln Lys Xaa Ala Gln Leu Cys Ile Xaa  
 1 5 10 15  
 Lys Val Cys Xaa Xaa Thr Xaa Xaa Arg  
 20 25

<210> 106  
 <211> 496  
 <212> DNA  
 <213> Conus consors

<220>  
 <221> CDS  
 <222> (21)..(242)

<400> 106  
 gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met  
 1 5 10



atg gtg tgg att aca gcc cct ctg tct gaa ggt ggt aaa ctg aac ggc 101  
Met Val Trp Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Gly  
15 20 25

gta att cgg ggt ttg gtg tca cac atc tta atc cca cag cat acc ttg 149  
Val Ile Arg Gly Leu Val Ser His Ile Leu Ile Pro Gln His Thr Leu  
30 35 40

cga agt ctg act tcc cgt gat cgt tct gac aac ggt ggt tcg agt gga 197  
Arg Ser Leu Thr Ser Arg Asp Arg Ser Asp Asn Gly Gly Ser Ser Gly  
45 50 55

gca caa ata tgc atc tgg aag gta tgt cca cca tcc cca tgg aaa 242  
Ala Gln Ile Cys Ile Trp Lys Val Cys Pro Pro Ser Pro Trp Lys  
60 65 70

tgaccacaag gaaaaagatg aacggcgtca gacaaccacc acaactgtag tgggacatcg 302

ttgatacgac ttcagcaaatt attttaacat cactgtggtc gtgaagaaat cagttgcttt 362

aaaagattgg atttttcctt gtttaagagt tgtactgata tcagctctgc actatgaaat 422

aaagctgatg tgacaaacaa aaaaaaaaaa aaaaaaagta ctctgcgttg ttactcgagc 482

ttaagggcga attc 496

<210> 107

<211> 74

<212> PRT

<213> Conus consors

<400> 107

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
1 5 10 15

Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Gly Val Ile Arg Gly Leu  
20 25 30

Val Ser His Ile Leu Ile Pro Gln His Thr Leu Arg Ser Leu Thr Ser  
35 40 45

Arg Asp Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile  
50 55 60

Trp Lys Val Cys Pro Pro Ser Pro Trp Lys  
65 70

<210> 108

<211> 25

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residues 16 and 24 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 20, 21 and 23 may be Pro or hydroxy-Pro

<400> 108

Asp Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile Xaa  
 1 5 10 15

Lys Val Cys Xaa Xaa Ser Xaa Xaa Lys  
 20 25

<210> 109

<211> 459

<212> DNA

<213> Conus coronatus

<220>

<221> CDS

<222> (1)..(240)

<400> 109

atg cag acg gcc tac tgg gtg atg atg atg atg atg gtg tgg att 48  
 Met Gln Thr Ala Tyr Trp Val Met Met Met Met Met Val Trp Ile  
 1 5 10 15

aca gcc cct ctg tct gaa ggt ggt aaa ctg aac gac gta att cgg ggt 96  
 Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly  
 20 25 30

ttg gtg cca gac gac tta acc cta cag cgt atg ttc aaa gct ctg gtt 144  
 Leu Val Pro Asp Asp Leu Thr Leu Gln Arg Met Phe Lys Ala Leu Val  
 35 40 45

tcc cat cgt ctt tct gac ggc aga gat tgg acg gga tac ata tgt atc 192  
 Ser His Arg Leu Ser Asp Gly Arg Asp Trp Thr Gly Tyr Ile Cys Ile  
 50 55 60

tgg aag gca tgt cca cgt ccc cca tgg atc cca cca aag gga aaa aga 240  
 Trp Lys Ala Cys Pro Arg Pro Pro Trp Ile Pro Pro Lys Gly Lys Arg  
 65 70 75 80

tgaatgacgt cagacaaccg ccacaactgt agtacgacat cgtaaacaca acttcagcta 300

atattttaac atcactgtgg ttgtgaagaa atcggttgct ttaaaagatt gaatttttcg 360

tttaagagtt gtgctgatac gagctctgca ctatgaaata aagctgatgt gacaaacaaa 420

aaaaaaaaa aaaaaaagta ctctgcgttg ttactcgag 459

<210> 110

<211> 80

<212> PRT

<213> Conus coronatus

<400> 110

Met Gln Thr Ala Tyr Trp Val Met Met Met Met Met Met Val Trp Ile  
 1 5 10 15  
 Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly  
 20 25 30

Leu Val Pro Asp Asp Leu Thr Leu Gln Arg Met Phe Lys Ala Leu Val  
 35 40 45

Ser His Arg Leu Ser Asp Gly Arg Asp Trp Thr Gly Tyr Ile Cys Ile  
 50 55 60

Trp Lys Ala Cys Pro Arg Pro Pro Trp Ile Pro Pro Lys Gly Lys Arg  
 65 70 75 80

<210> 111  
 <211> 26  
 <212> PRT  
 <213> Conus coronatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residues 7, 14 and 22 may be Trp or bromo-Trp; Xaa at residue 10 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 18, 29, 21, 24 and 25 may be Pro or hydroxy-Pro

<400> 111  
 Leu Ser Asp Gly Arg Asp Xaa Thr Gly Xaa Ile Cys Ile Xaa Lys Ala  
 1 5 10 15

Cys Xaa Arg Xaa Xaa Xaa Ile Xaa Xaa Lys  
 20 25

<210> 112  
 <211> 495  
 <212> DNA  
 <213> Conus ebraeus

<220>  
 <221> CDS  
 <222> (21)..(236)

<400> 112  
 gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg atg atg atg 53  
 Met Gln Thr Ala Tyr Trp Val Met Met Met Met  
 1 5 10

atg atg gtg tgg att aca gcc cct ctg tct gaa ggc ggt aaa ctg aac 101  
 Met Met Val Trp Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn  
 15 20 25

gac gta att cgg ggt ttg gtg cca gac gac tta acc cta cag cgt atg 149  
 Asp Val Ile Arg Gly Leu Val Pro Asp Asp Leu Thr Leu Gln Arg Met  
 30 35 40

ttc aaa agt ctg ttt tcc cat cgt ctt tct ggc ggc aca tat tcg agg 197  
 Phe Lys Ser Leu Phe Ser His Arg Leu Ser Gly Gly Thr Tyr Ser Arg  
 45 50 55

gta gac aca tgc atc tgg aag gta tgt cca caa tct cca tagggacgat 246  
 Val Asp Thr Cys Ile Trp Lys Val Cys Pro Gln Ser Pro  
 60 65 70

catatggaaa aagatgagt acatcagaca actgccacaa ctgtagtacg acatcggttaa 306

cacgacttca gctaataattt taacatcact gtggttgtga agaaatcggt tgctttaaaa 366

gattggattt ttccttgttt aagagttgtg ctgatatgag ctctgcacta tgaaataaag 426

ctgatgtgac aaacaaaaaa aaaaaaaaaa aagtactctg cgttgttact cgagcttaag 486

ggcgaattc

495

<210> 113  
 <211> 72  
 <212> PRT  
 <213> Conus ebraeus

<400> 113  
 Met Gln Thr Ala Tyr Trp Val Met Met Met Met Met Met Val Trp Ile  
 1 5 10 15  
 Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly  
 20 25 30  
 Leu Val Pro Asp Asp Leu Thr Leu Gln Arg Met Phe Lys Ser Leu Phe  
 35 40 45  
 Ser His Arg Leu Ser Gly Gly Thr Tyr Ser Arg Val Asp Thr Cys Ile  
 50 55 60  
 Trp Lys Val Cys Pro Gln Ser Pro  
 65 70

<210> 114  
 <211> 21  
 <212> PRT  
 <213> Conus ebraeus

<220>  
 <221> PEPTIDE  
 <222> (1)..(21)  
 <223> Xaa at residue 6 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr  
 , O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Trp (D  
 or L) or bromo-Trp (D or L); Xaa at residues 18 and 21 may be Pro  
 or hydroxy-Pro

<400> 114  
 Leu Ser Gly Gly Thr Xaa Ser Arg Val Asp Thr Cys Ile Xaa Lys Val  
 1 5 10 15  
 Cys Xaa Gln Ser Xaa  
 20

<210> 115  
 <211> 537  
 <212> DNA  
 <213> Conus geographus

<220>  
 <221> CDS  
 <222> (21)..(299)

<400> 115  
 gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg ctg atg atg 53  
 Met Gln Thr Ala Tyr Trp Val Met Leu Met Met  
 1 5 10

atg gtg tgc atc aca gcc cct ctg cct gaa ggt ggt aaa ccg aac agc 101  
 Met Val Cys Ile Thr Ala Pro Leu Pro Glu Gly Gly Lys Pro Asn Ser

15	20	25	
gga att cgg ggt ttg gtg cca aac gac tta act cca cag cat acc ttg			149
Gly Ile Arg Gly Leu Val Pro Asn Asp Leu Thr Pro Gln His Thr Leu			
30	35	40	
cga agt ctg att tcc cgt cgt caa act gac gtt ctt ctg gag gct acc			197
Arg Ser Leu Ile Ser Arg Arg Gln Thr Asp Val Leu Leu Glu Ala Thr			
45	50	55	
ctt ttg aca aca cca gcc ccc gag cag aga ttg ttc tgc ttc tgg aag			245
Leu Leu Thr Thr Pro Ala Pro Glu Gln Arg Leu Phe Cys Phe Trp Lys			
60	65	70	75
tca tgt acg tgg agg ccc tac cct tgg aga cga cgt gat ctt aat gga			293
Ser Cys Thr Trp Arg Pro Tyr Pro Trp Arg Arg Asp Leu Asn Gly			
80	85	90	
aaa cga tgaatgacgc cagacaaccg ccacaactgt agtacgacat cgttaatacg			349
Lys Arg			
acttcagcaa acattttaac ataactgtgg ttgtgaagaa atcagttgct ttaaaagatt			409
ggatttttcc ttgtttcaga gttgtactga tatgagctct gcaccatgaa ataaagctga			469
agtgacgaac aaaaaaaaaa aaaaaaaaaa agtactctgc gttgttactc gagcttaagg			529
gcgaattc			537
<210> 116			
<211> 93			
<212> PRT			
<213> Conus geographus			
<400> 116			
Met Gln Thr Ala Tyr Trp Val Met Leu Met Met Met Val Cys Ile Thr			
1	5	10	15
Ala Pro Leu Pro Glu Gly Gly Lys Pro Asn Ser Gly Ile Arg Gly Leu			
20	25	30	
Val Pro Asn Asp Leu Thr Pro Gln His Thr Leu Arg Ser Leu Ile Ser			
35	40	45	
Arg Arg Gln Thr Asp Val Leu Leu Glu Ala Thr Leu Leu Thr Thr Pro			
50	55	60	
Ala Pro Glu Gln Arg Leu Phe Cys Phe Trp Lys Ser Cys Thr Trp Arg			
65	70	75	80
Pro Tyr Pro Trp Arg Arg Arg Asp Leu Asn Gly Lys Arg			
85	90		
<210> 117			
<211> 40			
<212> PRT			
<213> Conus geographus			
<220>			

<221> PEPTIDE  
 <222> (1)..(40)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residues 7 and 17 may be Glu or Gla; Xaa at residues 14, 16, 31 and 33 may be Pro or hydroxy-Pro; Xaa at residues 24, 29 and 34 may be Trp (D or L) or bromo-Trp (D or L)

<220>  
 <221> PEPTIDE  
 <222> (1)..(40)  
 <223> Xaa at residue 32 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 117  
 Xaa Thr Asp Val Leu Leu Xaa Ala Thr Leu Leu Thr Thr Xaa Ala Xaa  
 1 5 10 15  
 Xaa Gln Arg Leu Phe Cys Phe Xaa Lys Ser Cys Thr Xaa Arg Xaa Xaa  
 20 25 30  
 Xaa Xaa Arg Arg Arg Asp Leu Asn  
 35 40

<210> 118  
 <211> 457  
 <212> DNA  
 <213> Conus gladiator

<220>  
 <221> CDS  
 <222> (1)..(246)

<400> 118  
 atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg gtt aca 48  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Val Thr  
 1 5 10 15  
 gtc cct cga tct gaa ggt ggc acg tgg aac tac tta att cgg ggt ttg 96  
 Val Pro Arg Ser Glu Gly Gly Thr Trp Asn Tyr Leu Ile Arg Gly Leu  
 20 25 30  
 gtg cca gac gac cta acc cca cag ctt acc ttg cat cgt ctg gtt acc 144  
 Val Pro Asp Asp Leu Thr Pro Gln Leu Thr Leu His Arg Leu Val Thr  
 35 40 45  
 cgt cgt cat cct gcc aac gtt aga cag cag ggg aaa ata tgt gta tgg 192  
 Arg Arg His Pro Ala Asn Val Arg Gln Gln Gly Lys Ile Cys Val Trp  
 50 55 60  
 aag gtg tgt cca cca tgg cca gta aga tca cct ggt cca cag cca aaa 240  
 Lys Val Cys Pro Pro Trp Pro Val Arg Ser Pro Gly Pro Gln Pro Lys  
 65 70 75 80  
 aac aaa tgacgtcaga caaccgccac aactttagta cgacatcggt gatacaactt 296  
 Asn Lys  
 cagcaagtat tttacatca ctgtggctct gaagaaatca gttgctttaa aagattggat 356  
 ttttccttgt tttagagttt tactgatatc agctctgcac tatgaaataa agatgtgacg 416

aaaaaaaaaa aaaaaaaaaag tactctgcgt tggtactcga g

457

<210> 119  
 <211> 82  
 <212> PRT  
 <213> Conus gladiator

<400> 119  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Val Thr  
 1 5 10 15  
 Val Pro Arg Ser Glu Gly Gly Thr Trp Asn Tyr Leu Ile Arg Gly Leu  
 20 25 30  
 Val Pro Asp Asp Leu Thr Pro Gln Leu Thr Leu His Arg Leu Val Thr  
 35 40 45  
 Arg Arg His Pro Ala Asn Val Arg Gln Gln Gly Lys Ile Cys Val Trp  
 50 55 60  
 Lys Val Cys Pro Pro Trp Pro Val Arg Ser Pro Gly Pro Gln Pro Lys  
 65 70 75 80

Asn Lys

<210> 120  
 <211> 32  
 <212> PRT  
 <213> Conus gladiator

<220>  
 <221> PEPTIDE  
 <222> (1)..(32)  
 <223> Xaa at residues 3, 18, 19, 21, 25, 27 and 29 may be Pro or hydrox  
 y-Pro; Xaa at residues 14 and 20 may be Trp (D or L) or bromo-Trp  
 (D or L)

<400> 120  
 His Xaa Ala Asn Val Arg Gln Gln Gly Lys Ile Cys Val Xaa Lys Val  
 1 5 10 15  
 Cys Xaa Xaa Xaa Xaa Val Arg Ser Xaa Gly Xaa Gln Xaa Lys Asn Lys  
 20 25 30

<210> 121  
 <211> 459  
 <212> DNA  
 <213> Conus gladiator

<220>  
 <221> CDS  
 <222> (1)..(246)

<400> 121  
 atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg gtt aca  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Val Thr  
 1 5 10 15  
 gtc cct cga tct gaa ggt ggc acg tgg aac tac tta att cgg ggt ttg  
 48 96

```

Val Pro Arg Ser Glu Gly Gly Thr Trp Asn Tyr Leu Ile Arg Gly Leu
      20              25              30

gtg cca gac gac cta acc cca cag ctt acc ttg cat cgt ctg gtt acc      144
Val Pro Asp Asp Leu Thr Pro Gln Leu Thr Leu His Arg Leu Val Thr
      35              40              45

cgt cgt cat cct gcc aac gtt aga cag cag ggg aaa ata tgt gta tgg      192
Arg Arg His Pro Ala Asn Val Arg Gln Gln Gly Lys Ile Cys Val Trp
      50              55              60

aag gtg tgt cca cca tcg cca gta aga tca cct ggt cca ctg cca aaa      240
Lys Val Cys Pro Pro Ser Pro Val Arg Ser Pro Gly Pro Leu Pro Lys
      65              70              75              80

aac aaa tgacgtcaga caaccgccac aacttttagta cgacatcggt gatacaactt      296
Asn Lys

cagcaagtat tttaacatca ctgtggctct gaagaaatca gttgctttaa aagattggat      356

ttttccttgt tttagagttt tactgatatc agctctgcac tatgaaataa agatgtgacg      416

gacaaaaaaaa aaaaaaaaaa agtactctgc gttgttactc gag                        459

<210> 122
<211> 82
<212> PRT
<213> Conus gladiator

<400> 122
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Val Thr
1              5              10              15

Val Pro Arg Ser Glu Gly Gly Thr Trp Asn Tyr Leu Ile Arg Gly Leu
      20              25              30

Val Pro Asp Asp Leu Thr Pro Gln Leu Thr Leu His Arg Leu Val Thr
      35              40              45

Arg Arg His Pro Ala Asn Val Arg Gln Gln Gly Lys Ile Cys Val Trp
      50              55              60

Lys Val Cys Pro Pro Ser Pro Val Arg Ser Pro Gly Pro Leu Pro Lys
      65              70              75              80

Asn Lys

<210> 123
<211> 32
<212> PRT
<213> Conus gladiator

<220>
<221> PEPTIDE
<222> (1)..(32)
<223> Xaa at residues 2, 18, 19, 21, 25, 27 and 29 may be Pro or hydrox
      y-Pro; Xaa at residue 14 may be Trp (D or L) or bromo-Trp (D or L
      )

```



&lt;400&gt; 123

His Xaa Ala Asn Val Arg Gln Gln Gly Lys Ile Cys Val Xaa Lys Val  
 1 5 10 15

Cys Xaa Xaa Ser Xaa Val Arg Ser Xaa Gly Xaa Leu Xaa Lys Asn Lys  
 20 25 30

&lt;210&gt; 124

&lt;211&gt; 499

&lt;212&gt; DNA

&lt;213&gt; Conus litoglyphus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (21)..(254)

&lt;400&gt; 124

gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met  
 1 5 10

atg gtg tgg att aca gcc cct ctg tct gaa ggt gat aaa ttg aac gac 101  
 Met Val Trp Ile Thr Ala Pro Leu Ser Glu Gly Asp Lys Leu Asn Asp  
 15 20 25

gta att cgg ggt ttg gtg cca gat aac tta gcc cca cag ctt gtt ttg 149  
 Val Ile Arg Gly Leu Val Pro Asp Asn Leu Ala Pro Gln Leu Val Leu  
 30 35 40

caa agt ctg gat tcc cgt cgt cat cct cac ggc att cgt cag gat gga 197  
 Gln Ser Leu Asp Ser Arg Arg His Pro His Gly Ile Arg Gln Asp Gly  
 45 50 55

gcc caa ata tgt atc tgg aag ata tgt cca cca tcc cca tgg aga cga 245  
 Ala Gln Ile Cys Ile Trp Lys Ile Cys Pro Pro Ser Pro Trp Arg Arg  
 60 65 70 75

ctt gga tct taagaaaaga aacaattgac gtcagacaac cgccacatct 294  
 Leu Gly Ser

tgagtagcagac atcgtaata cgacttcagc aaatatgaaa ttttcagcat cactgtggtt 354

gtgaagaaat cagttgcttt aaaagattgg atttgcctt gtttaagagt tgtactgatg 414

tcatctctgc actatgaaat aaagctgatg tgaaaaaaaa aaaaaaaagt actctgcggtt 474

gttactcgag cttaagggcg aattc 499

&lt;210&gt; 125

&lt;211&gt; 78

&lt;212&gt; PRT

&lt;213&gt; Conus litoglyphus

&lt;400&gt; 125

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15

Ala Pro Leu Ser Glu Gly Asp Lys Leu Asn Asp Val Ile Arg Gly Leu  
 20 25 30

Val Pro Asp Asn Leu Ala Pro Gln Leu Val Leu Gln Ser Leu Asp Ser  
                   35                                  40                                  45

Arg Arg His Pro His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile  
           50                                  55                                  60

Trp Lys Ile Cys Pro Pro Ser Pro Trp Arg Arg Leu Gly Ser  
   65                                  70                                  75

<210> 126

<211> 28

<212> PRT

<213> Conus litoglyphus

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residues 2, 19, 20 and 22 may be Pro or hydroxy-Pro; Xaa at residues 15 and 23 may be Trp (D or L) or bromo-Trp (D or L)

<400> 126

His Xaa His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile Xaa Lys  
   1                                  5                                  10                                  15

Ile Cys Xaa Xaa Ser Xaa Xaa Arg Arg Leu Gly Ser  
                   20                                  25

<210> 127

<211> 507

<212> DNA

<213> Conus litoglyphus

<220>

<221> CDS

<222> (21)..(254)

<400> 127

gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53  
                                   Met Gln Thr Ala Tyr Trp Val Met Val Met Met  
                                   1                                  5                                  10

atg gtg tgg att aca gcc cct ctg tct gaa ggt gat aaa ttg aac gac 101  
   Met Val Trp Ile Thr Ala Pro Leu Ser Glu Gly Asp Lys Leu Asn Asp  
                   15                                  20                                  25

gta att cgg ggt ttg gtg cca gat aac tta gcc cca cag ctt gtt ttg 149  
   Val Ile Arg Gly Leu Val Pro Asp Asn Leu Ala Pro Gln Leu Val Leu  
                   30                                  35                                  40

caa agt ctg gat tcc cgt cgt cat cct cac ggc att cgt cag gat gga 197  
   Gln Ser Leu Asp Ser Arg Arg His Pro His Gly Ile Arg Gln Asp Gly  
           45                                  50                                  55

gcc caa ata tgt atc tgg aag ata tgt cca cca tcc cca tgg aaa cga 245  
   Ala Gln Ile Cys Ile Trp Lys Ile Cys Pro Pro Ser Pro Trp Lys Arg  
   60                                  65                                  70                                  75

ctt gga tct taagaaaaga aacaattgac gtcagacaac cgccacaact 294  
   Leu Gly Ser

tgagtacgac atcgtaata caacttcagc aaatatgaaa ttttcagcat cactgtggtt 354  
 gtgaagaaat cagttgcttt aaaggattgg atttgcctt gtttaagagt tgtactgatg 414  
 tcattctctgc actatgaaat aaagctgatg tgacaagcaa aaaaaaaaaa aaaaaagtac 474  
 tctgcgttgt tactcgagct taagggcgaa ttc 507

<210> 128  
 <211> 78  
 <212> PRT  
 <213> Conus litoglyphus

<400> 128  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15  
 Ala Pro Leu Ser Glu Gly Asp Lys Leu Asn Asp Val Ile Arg Gly Leu  
 20 25 30  
 Val Pro Asp Asn Leu Ala Pro Gln Leu Val Leu Gln Ser Leu Asp Ser  
 35 40 45  
 Arg Arg His Pro His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile  
 50 55 60  
 Trp Lys Ile Cys Pro Pro Ser Pro Trp Lys Arg Leu Gly Ser  
 65 70 75

<210> 129  
 <211> 28  
 <212> PRT  
 <213> Conus litoglyphus

<220>  
 <221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residues 2, 19, 20 and 22 may be Pro or hydroxy-Pro; Xaa a  
 t residues 15 and 23 may be Trp (D or L) or bromo-Trp (D or L)

<400> 129  
 His Xaa His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile Xaa Lys  
 1 5 10 15  
 Ile Cys Xaa Xaa Ser Xaa Xaa Lys Arg Leu Gly Ser  
 20 25

<210> 130  
 <211> 507  
 <212> DNA  
 <213> Conus litteratus

<220>  
 <221> CDS  
 <222> (21)..(299)

<400> 130  
 gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53

[illegible]

<213> Conus litteratus

<220>

<221> PEPTIDE

<222> (1)..(50)

<223> Xaa at residues 2, 6, 8, 15, 20, 28 and 29 may be Pro or hydroxy-Pro; Xaa at residues 7 and 16 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 9 and 14 may be Glu or Glu

<220>

<221> PEPTIDE

<222> (1)..(50)

<223> Xaa at residue 24 may be Trp (D or L) or bromo-Trp (D or L)

<400> 132

Ser Xaa Val Ser Thr Xaa Xaa Xaa Xaa Phe His Leu Asp Xaa Xaa Xaa  
1 5 10 15

Leu Lys Ile Xaa Val Cys Ile Xaa Lys Ile Cys Xaa Xaa Asn Leu Leu  
20 25 30

Arg Arg Arg Asp Leu Lys Lys Arg Asn Lys Val Arg Gln Thr Thr Ala  
35 40 45

Thr Thr  
50

<210> 133

<211> 508

<212> DNA

<213> Conus litteratus

<220>

<221> CDS

<222> (21)..(275)

<400> 133

gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53  
Met Gln Thr Ala Tyr Trp Val Met Val Met Met  
1 5 10

atg gtg ggg att aca gcc cct ctg tct gaa ggt cgt aaa ttg aac gac 101  
Met Val Gly Ile Thr Ala Pro Leu Ser Glu Gly Arg Lys Leu Asn Asp  
15 20 25

gca att cgg ggt ttg gtg cca aat gac tta acc cca cag ctt ttg caa 149  
Ala Ile Arg Gly Leu Val Pro Asn Asp Leu Thr Pro Gln Leu Leu Gln  
30 35 40

agt ctg gtt tcc cgt cgt cat cgt gtg ttt cat ctt gac aac act tat 197  
Ser Leu Val Ser Arg Arg His Arg Val Phe His Leu Asp Asn Thr Tyr  
45 50 55

ctc aag ata ccc ata tgt gcc tgg aag gta tgt cca cca acc cca tgg 245  
Leu Lys Ile Pro Ile Cys Ala Trp Lys Val Cys Pro Pro Thr Pro Trp  
60 65 70 75

aga cga cgt gat ctt aag aaa aga aac aaa tgacgtcaga caaccgccac 295  
Arg Arg Arg Asp Leu Lys Lys Arg Asn Lys

80

85

aacttgagta cgacattggtt aatgcgactt gagcaaattt ttcagcatca ctatgggtgt 355  
 aaagaaatca gctgctttaa acgattggat ctttccttat ttaagagttg tattgatgtc 415  
 agctctgcac tctgaaataa agctgatgtg acaaacaaaa aaaaaaaaaa aaaaaagtac 475  
 tctgcgttgt tactcgagct taagggcgaa ttc 508

<210> 134  
 <211> 85  
 <212> PRT  
 <213> Conus litteratus

<400> 134  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Gly Ile Thr  
 1 5 10 15  
 Ala Pro Leu Ser Glu Gly Arg Lys Leu Asn Asp Ala Ile Arg Gly Leu  
 20 25 30  
 Val Pro Asn Asp Leu Thr Pro Gln Leu Leu Gln Ser Leu Val Ser Arg  
 35 40 45  
 Arg His Arg Val Phe His Leu Asp Asn Thr Tyr Leu Lys Ile Pro Ile  
 50 55 60  
 Cys Ala Trp Lys Val Cys Pro Pro Thr Pro Trp Arg Arg Arg Asp Leu  
 65 70 75 80  
 Lys Lys Arg Asn Lys  
 85

<210> 135  
 <211> 36  
 <212> PRT  
 <213> Conus litteratus

<220>  
 <221> PEPTIDE  
 <222> (1)..(36)  
 <223> Xaa at residue 10 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,  
 r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 14, 22, 23 and  
 25 may be Pro or hydroxy-Pro; Xaa at residues 18 and 26 may be Trp  
 (D or L) or bromo-Trp (D or L)

<400> 135  
 His Arg Val Phe His Leu Asp Asn Thr Xaa Leu Lys Ile Xaa Ile Cys  
 1 5 10 15  
 Ala Xaa Lys Val Cys Xaa Xaa Thr Xaa Xaa Arg Arg Arg Asp Leu Lys  
 20 25 30  
 Lys Arg Asn Lys  
 35

<210> 136  
 <211> 498  
 <212> DNA  
 <213> Conus loroisii

```

<220>
<221> CDS
<222> (21)..(236)
<220>
<221> misc_feature
<222> (1)..(498)
<223> n may be any base

<400> 136
gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg      53
                Met Gln Thr Ala Tyr Trp Val Met Val Met Met
                1                5                10

atg gtg tgg att aaa ggc cct gtg tct gaa ggt ggt aaa ttg aac gac      101
Met Val Trp Ile Lys Gly Pro Val Ser Glu Gly Gly Lys Leu Asn Asp
                15                20                25

gta att cgg ggt ttg gtg cca gac gac tta acc cca cag ctt atc ttg      149
Val Ile Arg Gly Leu Val Pro Asp Asp Leu Thr Pro Gln Leu Ile Leu
                30                35                40

caa agt ctg atg tcc cgt cgt cgt tct gac agc gat gtt cgg gag gtg      197
Gln Ser Leu Met Ser Arg Arg Arg Ser Asp Ser Asp Val Arg Glu Val
                45                50                55

tac ata tta tgc atc tgg aag ata tgt cca cca ttg cca tgaagacgac      246
Tyr Ile Leu Cys Ile Trp Lys Ile Cys Pro Pro Leu Pro
                60                65                70

atgatcttaa ggaaaaggat aaacgacgtc agacaaccgc tacaactgta gtacgacatc      306

gttaatacga cttcagcaaa tatttgaaca tcactgtggt tgtgaagaaa tcagttgott      366

taaacgattg gatttttcct taagagttgc actgatatca gctctgcact atgaaataaa      426

gctgatgtga ctacaaaaaa aaaaaaaaaa aaaaagtact ntgcgttggt actcgagctt      486

aagggcgaat tc                                                         498

<210> 137
<211> 72
<212> PRT
<213> Conus loroisii

<400> 137
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Lys
1                5                10                15

Gly Pro Val Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
20                25                30

Val Pro Asp Asp Leu Thr Pro Gln Leu Ile Leu Gln Ser Leu Met Ser
35                40                45

Arg Arg Arg Ser Asp Ser Asp Val Arg Glu Val Tyr Ile Leu Cys Ile
50                55                60

Trp Lys Ile Cys Pro Pro Leu Pro
65                70

```

<210> 138  
 <211> 22  
 <212> PRT  
 <213> Conus loroisii  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa at residue 8 may be Glu or Gla; Xaa at residue 10 may be Tyr,  
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-  
 Tyr; Xaa at residue 15 may be Trp (D or L) or bromo-Trp (D or L);  
 Xaa at residues 19, 20 and 22 may be Pro or hydroxy-Pro

<400> 138  
 Arg Ser Asp Ser Asp Val Arg Xaa Val Xaa Ile Leu Cys Ile Xaa Lys  
 1 5 10 15  
 Ile Cys Xaa Xaa Leu Xaa  
 20

<210> 139  
 <211> 495  
 <212> DNA  
 <213> Conus magus

<220>  
 <221> CDS  
 <222> (21)..(242)

<400> 139  
 gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met  
 1 5 10  
 atg gtg tgg att aca gcc cct ctg tct gaa ggt ggt aaa ttg aac gac 101  
 Met Val Trp Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp  
 15 20 25  
 gta att cgg ggt ttg gtg cca cac tcc tta acc cca cag cat atc ttg 149  
 Val Ile Arg Gly Leu Val Pro His Ser Leu Thr Pro Gln His Ile Leu  
 30 35 40  
 caa agt ctg act tcc cgt aat ggt tct ggc agc agc aat cag aaa gaa 197  
 Gln Ser Leu Thr Ser Arg Asn Gly Ser Gly Ser Ser Asn Gln Lys Glu  
 45 50 55  
 gca caa cta tgc atc tgg aag gta tgt cca cca tcc cca tgg aga 242  
 Ala Gln Leu Cys Ile Trp Lys Val Cys Pro Pro Ser Pro Trp Arg  
 60 65 70  
 tgaccacaag gaaaaagatg aacggcgtca gacaaccgcc acaactgtag tgggacatcg 302  
 ttgatacgac ttcaacaaat attttaacat cactgtgggt gtaaagaaat cagttgcttt 362  
 aaaagattgg atttttcctt gtttaagagt tgtactgata tcagctctgc actatgaaat 422  
 aaagctgatg tgacaaacaa aaaaaaaaaa aaaaaagtac tctgcgttgt tactcgagct 482  
 taagggcgaa ttc 495



<210> 140  
 <211> 74  
 <212> PRT  
 <213> Conus magus

<400> 140  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15  
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu  
 20 25 30  
 Val Pro His Ser Leu Thr Pro Gln His Ile Leu Gln Ser Leu Thr Ser  
 35 40 45  
 Arg Asn Gly Ser Gly Ser Ser Asn Gln Lys Glu Ala Gln Leu Cys Ile  
 50 55 60  
 Trp Lys Val Cys Pro Pro Ser Pro Trp Arg  
 65 70

<210> 141  
 <211> 25  
 <212> PRT  
 <213> Conus magus

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 10 may be Glu or Gla; Xaa at residues 16 and 24 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 20, 21 and 23 may be Pro or hydroxy-Pro

<400> 141  
 Asn Gly Ser Gly Ser Ser Asn Gln Lys Xaa Ala Gln Leu Cys Ile Xaa  
 1 5 10 15  
 Lys Val Cys Xaa Xaa Ser Xaa Xaa Arg  
 20 25

<210> 142  
 <211> 587  
 <212> DNA  
 <213> Conus miles

<220>  
 <221> CDS  
 <222> (21)..(347)

<220>  
 <221> misc\_feature  
 <222> (1)..(587)  
 <223> n may be any nucleotide

<400> 142  
 gaattcgcccc ttatggatcc atg cag acg gcc tac tgg gtg atg atg atg gtg 53  
 Met Gln Thr Ala Tyr Trp Val Met Met Met Val  
 1 5 10  
 gtg atg atg gtg ggg gtt act gtc gct ggc tcc ctg cct gtg ttt gat 101

Val Met Met Val Gly Val Thr Val Ala Gly Ser Leu Pro Val Phe Asp  
 15 20 25

gac gac aac gac tct gac ccc gct gtc aag cgc gct atc acg tgg tcc 149  
 Asp Asp Asn Asp Ser Asp Pro Ala Val Lys Arg Ala Ile Thr Trp Ser  
 30 35 40

cgc atc ctg ggc gtg tct cca gcc ttc ctg gca cag cag cga gcg ctg 197  
 Arg Ile Leu Gly Val Ser Pro Ala Phe Leu Ala Gln Gln Arg Ala Leu  
 45 50 55

gtt ccc ttc gcc aac cga ttc atc agt gag cag aaa cgt ttc cga ccc 245  
 Val Pro Phe Ala Asn Arg Phe Ile Ser Glu Gln Lys Arg Phe Arg Pro  
 60 65 70 75

gcc atg cag agc cga tca gga gga atg tgc ctg tgc cta tgg aaa gtg 293  
 Ala Met Gln Ser Arg Ser Gly Gly Met Ser Leu Cys Leu Trp Lys Val  
 80 85 90

tgt cct gca gcc ccc tgg ctg gtc gcc aaa cgt aaa cag gaa acc agc 341  
 Cys Pro Ala Ala Pro Trp Leu Val Ala Lys Arg Lys Gln Glu Thr Ser  
 95 100 105

gac tac tgacgtcata cctctaaaga cccactcatg acgtcaacgc tgaactgacg 397  
 Asp Tyr

tcaccgacag ctccaacgtc acagcaggag cgagagagag gctggagcat ttctctttct 457

tttgggtttt cgagttgaag tgtgatcagc tgggctggtg aaaaaattgt tgagtaaagt 517

tgaatgaaaa tcaaaaaaaaa aaaaaaaaaa agtactctgc gttggtactc gaggcttaaa 577

ggcgnaattc 587

<210> 143  
 <211> 109  
 <212> PRT  
 <213> Conus miles

<400> 143  
 Met Gln Thr Ala Tyr Trp Val Met Met Met Val Val Met Met Val Gly  
 1 5 10 15

Val Thr Val Ala Gly Ser Leu Pro Val Phe Asp Asp Asp Asn Asp Ser  
 20 25 30

Asp Pro Ala Val Lys Arg Ala Ile Thr Trp Ser Arg Ile Leu Gly Val  
 35 40 45

Ser Pro Ala Phe Leu Ala Gln Gln Arg Ala Leu Val Pro Phe Ala Asn  
 50 55 60

Arg Phe Ile Ser Glu Gln Lys Arg Phe Arg Pro Ala Met Gln Ser Arg  
 65 70 75 80

Ser Gly Gly Met Ser Leu Cys Leu Trp Lys Val Cys Pro Ala Ala Pro  
 85 90 95

Trp Leu Val Ala Lys Arg Lys Gln Glu Thr Ser Asp Tyr

100

105

<210> 144  
 <211> 37  
 <212> PRT  
 <213> Conus miles

<220>  
 <221> PEPTIDE  
 <222> (1)..(37)  
 <223> Xaa at residues 3, 21 and 24 may be Pro or hydroxy-Pro; Xaa at residues 17 and 25 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residue 33 may be Glu or Glu;

<220>  
 <221> PEPTIDE  
 <222> (1)..(37)  
 <223> Xaa at residue 37 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 144  
 Phe Arg Xaa Ala Met Gln Ser Arg Ser Gly Gly Met Ser Leu Cys Leu  
 1 5 10 15

Xaa Lys Val Cys Xaa Ala Ala Xaa Xaa Leu Val Ala Lys Arg Lys Gln  
 20 25 30

Xaa Thr Ser Asp Xaa  
 35

<210> 145  
 <211> 499  
 <212> DNA  
 <213> Conus miles

<220>  
 <221> CDS  
 <222> (21)..(401)

<400> 145  
 gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met  
 1 5 10

atg gtg gtg ggt tca ccg tcg gga gtc acg tcc atc ggt ctc aca gtc 101  
 Met Val Val Gly Ser Pro Ser Gly Val Thr Ser Ile Gly Leu Thr Val  
 15 20 25

cta cgt cgc gca acc atg gtg atg act cca ttc atg aca aga cga ttc 149  
 Leu Arg Arg Ala Thr Met Val Met Thr Pro Phe Met Thr Arg Arg Phe  
 30 35 40

atc aac atc tgt ttg ccc gtc ttc ctc tgg aga aca acg acg acc atc 197  
 Ile Asn Ile Cys Leu Pro Val Phe Leu Trp Arg Thr Thr Thr Thr Ile  
 45 50 55

gtt ctg tgg atc ttc ctg cag tgt atg cgc cgg gcc agg cac gtg tgc 245  
 Val Leu Trp Ile Phe Leu Gln Cys Met Arg Arg Ala Arg His Val Cys  
 60 65 70 75

gtt cta ctt ttg ttc ttg acc tca ttg cag ata ggg gtt ggt gca gac 293  
 Val Leu Leu Leu Phe Leu Thr Ser Leu Gln Ile Gly Val Gly Ala Asp  
                   80                  85                  90

gac atg aaa cta cag cgc caa aga cgt caa ggt ttc tgt tgc gtc gtt 341  
 Asp Met Lys Leu Gln Arg Gln Arg Arg Gln Gly Phe Cys Cys Val Val  
                   95                  100                  105

atc ccg att ctt tgg ttc tgt tgt ggg ggt tac cgc aca aat ggc act 389  
 Ile Pro Ile Leu Trp Phe Cys Cys Gly Gly Tyr Arg Thr Asn Gly Thr  
                   110                  115                  120

gca ctg gcc gat tgaaagaact gcaataaacg gaatggcaag aaggaataaa 441  
 Ala Leu Ala Asp  
                   125

aaaaaaaaaa aaaaaaaaaa agtactctgc gttgttactc gagcttaagg gcgaattc 499

<210> 146  
 <211> 127  
 <212> PRT  
 <213> Conus miles

<400> 146  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Val Gly Ser  
 1                  5                  10                  15  
 Pro Ser Gly Val Thr Ser Ile Gly Leu Thr Val Leu Arg Arg Ala Thr  
                   20                  25                  30  
 Met Val Met Thr Pro Phe Met Thr Arg Arg Phe Ile Asn Ile Cys Leu  
                   35                  40                  45  
 Pro Val Phe Leu Trp Arg Thr Thr Thr Thr Ile Val Leu Trp Ile Phe  
                   50                  55                  60  
 Leu Gln Cys Met Arg Arg Ala Arg His Val Cys Val Leu Leu Leu Phe  
 65                  70                  75                  80  
 Leu Thr Ser Leu Gln Ile Gly Val Gly Ala Asp Asp Met Lys Leu Gln  
                   85                  90                  95  
 Arg Gln Arg Arg Gln Gly Phe Cys Cys Val Val Ile Pro Ile Leu Trp  
                   100                  105                  110  
 Phe Cys Cys Gly Gly Tyr Arg Thr Asn Gly Thr Ala Leu Ala Asp  
                   115                  120                  125

<210> 147  
 <211> 27  
 <212> PRT  
 <213> Conus miles

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 9 may be Pro  
 or hydroxy-Pro; Xaa at residue 12 may be Trp (D or L) or bromo-Trp  
 p(D or L); Xaa at residue 18 may be Tyr, 125I-Tyr, mono-iodo-Tyr,  
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

&lt;400&gt; 147

Xaa Gly Phe Cys Cys Val Val Ile Xaa Ile Leu Xaa Phe Cys Cys Gly  
 1 5 10 15

Gly Xaa Arg Thr Asn Gly Thr Ala Leu Ala Asp  
 20 25

&lt;210&gt; 148

&lt;211&gt; 450

&lt;212&gt; DNA

<213> *Conus muriculatus*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(237)

&lt;400&gt; 148

atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15

gcc cct ttg tct gaa ggt ggt aaa ctg aac gat gta att cgg ggt ttc 96  
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Phe  
 20 25 30

gcg cta gat gac tta gcc caa agc cgt att atg caa agt ctg gtt ttc 144  
 Ala Leu Asp Asp Leu Ala Gln Ser Arg Ile Met Gln Ser Leu Val Phe  
 35 40 45

agt cat cag cct ctt cca acg gca tcc ata tgt atc tgg aag ata tgt 192  
 Ser His Gln Pro Leu Pro Thr Ala Ser Ile Cys Ile Trp Lys Ile Cys  
 50 55 60

cca cca gac cca tgg aga cga cat gat ctt cag aaa agt aac aaa 237  
 Pro Pro Asp Pro Trp Arg Arg His Asp Leu Gln Lys Ser Asn Lys  
 65 70 75

tgacgtcaga caaccgccac aacttgaata caacatcatt aatacgactt cagcaaatat 297

tttaacatca ctgtgattgt tcggaagtca gttgctttaa aggattggat ttgtccctgt 357

tgtattgatg tcaactctgc actatgaaat aaagctgatg tgacaaacaa gaaaaaaaaa 417

aaaaaaaaaa agtactctgc gttgttactc gag 450

&lt;210&gt; 149

&lt;211&gt; 79

&lt;212&gt; PRT

<213> *Conus muriculatus*

&lt;400&gt; 149

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15

Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Phe  
 20 25 30

Ala Leu Asp Asp Leu Ala Gln Ser Arg Ile Met Gln Ser Leu Val Phe  
 35 40 45

Ser His Gln Pro Leu Pro Thr Ala Ser Ile Cys Ile Trp Lys Ile Cys  
50 55 60

Pro Pro Asp Pro Trp Arg Arg His Asp Leu Gln Lys Ser Asn Lys  
65 70 75

<210> 150

<211> 38

<212> PRT

<213> Conus muriculatus

<220>

<221> PEPTIDE

<222> (1)..(38)

<223> Xaa at residues 11, 13, 24, 25 and 27 may be Pro or hydroxy-Pro;  
Xaa at residue 20 and 28 may be Trp or bromo-Trp

<400> 150

Ile Met Gln Ser Leu Val Phe Ser His Gln Xaa Leu Xaa Thr Ala Ser  
1 5 10 15

Ile Cys Ile Xaa Lys Ile Cys Xaa Xaa Asp Xaa Xaa Arg Arg His Asp  
20 25 30

Leu Gln Lys Ser Asn Lys  
35

<210> 151

<211> 437

<212> DNA

<213> Conus musicus

<220>

<221> CDS

<222> (1)..(240)

<400> 151

atg cag acg gcc tac tgg gtg atg atg atg acg atg atg gtg tgg atg 48  
Met Gln Thr Ala Tyr Trp Val Met Met Met Thr Met Met Val Trp Met  
1 5 10 15

aca gcc cct ctg tct gaa ggt cgt cca ctg agc gac gaa gtt cgg ggt 96  
Thr Ala Pro Leu Ser Glu Gly Arg Pro Leu Ser Asp Glu Val Arg Gly  
20 25 30

atg gtg cca ggc gac ttg gtc cta cag tat ctg ttc cca agt ctg gct 144  
Met Val Pro Gly Asp Leu Val Leu Gln Tyr Leu Phe Pro Ser Leu Ala  
35 40 45

ttc agt cct ccg gac ata tgt acg tgg aag gta tgt cca cca ccc cca 192  
Phe Ser Pro Pro Asp Ile Cys Thr Trp Lys Val Cys Pro Pro Pro Pro  
50 55 60

tgg aga cga cca aaa aaa ata aca gac gtc aga cag ccg cca caa ctg 240  
Trp Arg Arg Pro Lys Lys Ile Thr Asp Val Arg Gln Pro Pro Gln Leu  
65 70 75 80

tagtacgaca tcgttgatac ggcttcagca aatattttca acatcactgc gggtgtgaag 300

aaatcagttg ctttaaaatg ttggattttt ccttggttttaa aagagctgta ctgatgtcag 360

ccctgcatta cgaaataaag ctgatgtgac aaacaaaaaa aaaaaaaaaa aaaaagtact 420

ctgcgttggt actcgag 437

<210> 152

<211> 80

<212> PRT

<213> Conus musicus

<400> 152

Met Gln Thr Ala Tyr Trp Val Met Met Met Thr Met Met Val Trp Met  
1 5 10 15

Thr Ala Pro Leu Ser Glu Gly Arg Pro Leu Ser Asp Glu Val Arg Gly  
20 25 30

Met Val Pro Gly Asp Leu Val Leu Gln Tyr Leu Phe Pro Ser Leu Ala  
35 40 45

Phe Ser Pro Pro Asp Ile Cys Thr Trp Lys Val Cys Pro Pro Pro Pro  
50 55 60

Trp Arg Arg Pro Lys Lys Ile Thr Asp Val Arg Gln Pro Pro Gln Leu  
65 70 75 80

<210> 153

<211> 49

<212> PRT

<213> Conus musicus

<220>

<221> PEPTIDE

<222> (1)..(49)

<223> Xaa at residues 4, 14, 20, 21, 30, 31, 32, 33, 37, 46 and 47 may be Pro or hydroxy-Pro; Xaa at residue 11 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 26 and 34 may be Trp (D or L) or bromo-Trp (D or L)

<400> 153

Gly Met Val Xaa Gly Asp Leu Val Leu Gln Xaa Leu Phe Xaa Ser Leu  
1 5 10 15

Ala Phe Ser Xaa Xaa Asp Ile Cys Thr Xaa Lys Val Cys Xaa Xaa Xaa  
20 25 30

Xaa Xaa Arg Arg Xaa Lys Lys Ile Thr Asp Val Arg Gln Xaa Xaa Gln  
35 40 45

Leu

<210> 154

<211> 436

<212> DNA

<213> Conus musicus

<220>

<221> CDS

<222> (1)..(216)

<400> 154  
 atg cag acg gcc tac tgg gtg atg atg atg atg atg atg gtg tgg atg 48  
 Met Gln Thr Ala Tyr Trp Val Met Met Met Met Met Met Val Trp Met  
 1 5 10 15  
 aca gcc cct ctg tct gaa ggt cgt aaa ctg atc gac aaa gtt cgg ggt 96  
 Thr Ala Pro Leu Ser Glu Gly Arg Lys Leu Ile Asp Lys Val Arg Gly  
 20 25 30  
 atg ggg cca ggc gac tta tcc cta cag aaa atg ttc cca agt ctg gct 144  
 Met Gly Pro Gly Asp Leu Ser Leu Gln Lys Met Phe Pro Ser Leu Ala  
 35 40 45  
 tta ggt cct ggg gga gac gta ata tgt agg tgg aag gta tgt cca cca 192  
 Leu Gly Pro Gly Gly Asp Val Ile Cys Arg Trp Lys Val Cys Pro Pro  
 50 55 60  
 acc cca tgg aaa cga cta ata aaa taactgacgt cagacagccg ccacaactgt 246  
 Thr Pro Trp Lys Arg Leu Ile Lys  
 65 70  
 agtacgacat cgttgatacg acttcagcaa atatttcaac atcactgcgg ttgtgaagaa 306  
 atcagttgct ttaaaagatt ggatttttcc ttgttttaaag agttgtactg atatcagctc 366  
 tgcattacga aataaagctg atgtgacaaa caaaaaaaaaa aaaaaaaagt actctgcggt 426  
 gttactcgag 436

<210> 155  
 <211> 72  
 <212> PRT  
 <213> Conus musicus

<400> 155  
 Met Gln Thr Ala Tyr Trp Val Met Met Met Met Met Met Val Trp Met  
 1 5 10 15  
 Thr Ala Pro Leu Ser Glu Gly Arg Lys Leu Ile Asp Lys Val Arg Gly  
 20 25 30  
 Met Gly Pro Gly Asp Leu Ser Leu Gln Lys Met Phe Pro Ser Leu Ala  
 35 40 45  
 Leu Gly Pro Gly Gly Asp Val Ile Cys Arg Trp Lys Val Cys Pro Pro  
 50 55 60  
 Thr Pro Trp Lys Arg Leu Ile Lys  
 65 70

<210> 156  
 <211> 41  
 <212> PRT  
 <213> Conus musicus

<220>  
 <221> PEPTIDE  
 <222> (1)..(41)  
 <223> Xaa at residues 4, 14, 20, 32, 33 and 35 may be Pro or hydroxy-Pr  
 o; Xaa at residues 28 and 36 may be Trp (D or L) or bromo-Trp (D



or L)

<400> 156

Gly Met Gly Xaa Gly Asp Leu Ser Leu Gln Lys Met Phe Xaa Ser Leu  
1 5 10 15

Ala Leu Gly Xaa Gly Gly Asp Val Ile Cys Arg Xaa Lys Val Cys Xaa  
20 25 30

Xaa Thr Xaa Xaa Lys Arg Leu Ile Lys  
35 40

<210> 157

<211> 449

<212> DNA

<213> Conus musicus

<220>

<221> CDS

<222> (1)..(243)

<400> 157

atg cag acg gcc tac tgg gtg atg atg atg atg acg atg atg gtg tgg 48  
Met Gln Thr Ala Tyr Trp Val Met Met Met Met Thr Met Met Val Trp  
1 5 10 15

atg aca gcc cct ctg tct gaa ggt cgt cca ctg agc gac aaa gtt cgg 96  
Met Thr Ala Pro Leu Ser Glu Gly Arg Pro Leu Ser Asp Lys Val Arg  
20 25 30

ggt atg gtg cca ggc gac tta gcc ctg cag tat ctg ttc cca agt ctg 144  
Gly Met Val Pro Gly Asp Leu Ala Leu Gln Tyr Leu Phe Pro Ser Leu  
35 40 45

gct ttc aat ccc ccg gac ata tgt acg tgg aag gta tgt cca cca ccc 192  
Ala Phe Asn Pro Pro Asp Ile Cys Thr Trp Lys Val Cys Pro Pro Pro  
50 55 60

cca tgg aga cga cca aaa aaa ata act gac gtc gga cag ccg cca caa 240  
Pro Trp Arg Arg Pro Lys Lys Ile Thr Asp Val Gly Gln Pro Pro Gln  
65 70 75 80

ctg tagtacgaca tcgttgatac gacttcagca aatattttca acatcactgc 293  
Leu

ggttgtgaag aaatcagttg ttttaaaagg ttggattttt ccttgtttaa aagagctgta 353

ctgatgtcag ctctgcatta cgaaataaag ctgatgtgac aaacgaaaaa aaaaaaaaaa 413

aaaaaaaaaa aaaagtactc tgcgttggtta ctcgag 449

<210> 158

<211> 81

<212> PRT

<213> Conus musicus

<400> 158

Met Gln Thr Ala Tyr Trp Val Met Met Met Met Thr Met Met Val Trp  
1 5 10 15

Met Thr Ala Pro Leu Ser Glu Gly Arg Pro Leu Ser Asp Lys Val Arg  
20 25 30

Gly Met Val Pro Gly Asp Leu Ala Leu Gln Tyr Leu Phe Pro Ser Leu  
35 40 45

Ala Phe Asn Pro Pro Asp Ile Cys Thr Trp Lys Val Cys Pro Pro Pro  
50 55 60

Pro Trp Arg Arg Pro Lys Lys Ile Thr Asp Val Gly Gln Pro Pro Gln  
65 70 75 80

Leu

<210> 159

<211> 49

<212> PRT

<213> Conus musicus

 $\langle 220 \rangle$ 

&lt;221&gt; PEPTIDE

<222> (1) . . (49)

<223> Xaa at residues 4, 14, 20, 21, 30, 31, 32, 33, 37, 46 and 47 may be Pro or hydroxy-Pro; Xaa at residue 11 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 26 and 34 may be Trp (D or L) or bromo-Trp (D or L)

<400> 159

Gly Met Val Xaa Gly Asp Leu Ala Leu Gln Xaa Leu Phe Xaa Ser Leu  
1 5 10 15

Ala Phe Asn Xaa Xaa Asp Ile Cys Thr Xaa Lys Val Cys Xaa Xaa Xaa  
20 25 30

Xaa Xaa Arg Arg Xaa Lys Lys Ile Thr Asp Val Gly Gln Xaa Xaa Gln  
35 40 45

Leu

$\langle 210 \rangle$  160

<211> 436

<212> DNA

<213> Conus musicus

 $\langle 220 \rangle$ 

<221> CDS

 $\langle 222 \rangle \quad (1) \dots (240)$ 

$\langle 400 \rangle$  160

atg cag acg gcc tac tgg gtg atg atg atg acg atg atg gtg tgg atg 48  
Met Gln Thr Ala Tyr Trp Val Met Met Met Thr Met Met Val Trp Met  
1 5 10 15

aca gcc cct ctg tct gaa ggt cgt cca ctg agc gac aaa gtt cgg ggt 96  
Thr Ala Pro Leu Ser Glu Gly Arg Pro Leu Ser Asp Lys Val Arg Gly  
20 25 30

atg gtg cca ggc gac tta gtc ctg cag tat ctg ttc cca agt ctg gct 144  
Met Val Pro Gly Asp Leu Val Leu Gln Tyr Leu Phe Pro Ser Leu Ala

```

          35              40              45
ttc aat cct ccg gac ata tgt acg tgg aag gta tgt cca cca ccc cca      192
Phe Asn Pro Pro Asp Ile Cys Thr Trp Lys Val Cys Pro Pro Pro Pro
    50              55              60

tgg aga cga cca aaa aaa ata act gac gtc aga cag ccg cca caa ctg      240
Trp Arg Arg Pro Lys Lys Ile Thr Asp Val Arg Gln Pro Pro Gln Leu
    65              70              75              80

tagtacgaca tcgttgatac gacttcagca aatattttca acatcactgc ggttgtgaag      300

aaatcagttg ttttaaaagg ttggattttt ccttgtttaa aagagctgta ctgatgtcag      360

ctctgcatta cgaaataaag ctgatgtgac aagcaaaaaa aaaaaaaaaa aaaagtactc      420

tgcgttggtta ctcgag                                                    436

```

```

<210> 161
<211> 80
<212> PRT
<213> Conus musicus

```

```

<400> 161
Met Gln Thr Ala Tyr Trp Val Met Met Met Thr Met Met Val Trp Met
1              5              10              15

Thr Ala Pro Leu Ser Glu Gly Arg Pro Leu Ser Asp Lys Val Arg Gly
          20              25              30

Met Val Pro Gly Asp Leu Val Leu Gln Tyr Leu Phe Pro Ser Leu Ala
          35              40              45

Phe Asn Pro Pro Asp Ile Cys Thr Trp Lys Val Cys Pro Pro Pro Pro
    50              55              60

Trp Arg Arg Pro Lys Lys Ile Thr Asp Val Arg Gln Pro Pro Gln Leu
    65              70              75              80

```

```

<210> 162
<211> 49
<212> PRT
<213> Conus musicus

```

```

<220>
<221> PEPTIDE
<222> (1)..(49)
<223> Xaa at residues 4, 14, 20, 21, 30, 31, 32, 33, 37, 46 and 47 may
      be Pro or hydroxy-Pro; Xaa at residue 11 may be Tyr, 125I-Tyr, mo
      no-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at r
      esidues 26 and 34 may be Trp (D or L) or bromo-Trp (D or L)

```

```

<400> 162
Gly Met Val Xaa Gly Asp Leu Val Leu Gln Xaa Leu Phe Xaa Ser Leu
1              5              10              15

Ala Phe Asn Xaa Xaa Asp Ile Cys Thr Xaa Lys Val Cys Xaa Xaa Xaa
          20              25              30

Xaa Xaa Arg Arg Xaa Lys Lys Ile Thr Asp Val Arg Gln Xaa Xaa Gln

```

```

35                               40                               45

Leu

<210> 163
<211> 462
<212> DNA
<213> Conus mustelinus

<220>
<221> CDS
<222> (1)..(225)

<400> 163
atg cag acg gcc tac tgg gtg atg gtg atg atg atg gcg tgg tat aca      48
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Ala Trp Tyr Thr
1                               5                               10                               15
acc cct gtg tct gaa tgt ggg aaa ttg aac aac gta att cgg ggt ttt      96
Thr Pro Val Ser Glu Cys Gly Lys Leu Asn Asn Val Ile Arg Gly Phe
20                               25                               30

gtg cca aag gac tgg acc cca atg ctt ccc tgg cgt cgt cta gtt tcc      144
Val Pro Lys Asp Trp Thr Pro Met Leu Pro Trp Arg Arg Leu Val Ser
35                               40                               45

cat acc agc agc aag tat cca ggt gtg act ttt tgt cca tgg aag gtg      192
His Thr Ser Ser Lys Tyr Pro Gly Val Thr Phe Cys Pro Trp Lys Val
50                               55                               60

tgt ccg cca gcg cca tgg aga ata ctt ggg gtc taacgcaaaa aaatacatga      245
Cys Pro Pro Ala Pro Trp Arg Ile Leu Gly Val
65                               70                               75

cgtcagacaa cgcgccaccgc tttagtagca catcggtcat acgtctccag caagtatttt      305

aacatcactg tggttgtgaa gaagtcagta gctttaaaag attggatttt ttccottgttt      365

aagagttgta ctgacatgag ttctgcacta tgaaataaag ttgatgtgac gaacgaaaaa      425

aaaaaaaaaa aaaaagtact ctgcgttggtt actcgag                                462

<210> 164
<211> 75
<212> PRT
<213> Conus mustelinus

<400> 164
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Ala Trp Tyr Thr
1                               5                               10                               15

Thr Pro Val Ser Glu Cys Gly Lys Leu Asn Asn Val Ile Arg Gly Phe
20                               25                               30

Val Pro Lys Asp Trp Thr Pro Met Leu Pro Trp Arg Arg Leu Val Ser
35                               40                               45

His Thr Ser Ser Lys Tyr Pro Gly Val Thr Phe Cys Pro Trp Lys Val
50                               55                               60

Cys Pro Pro Ala Pro Trp Arg Ile Leu Gly Val

```

65 70 75

<210> 165  
 <211> 30  
 <212> PRT  
 <213> *Conus mustelinus*

<220>  
 <221> PEPTIDE  
 <222> (1)..(30)  
 <223> Xaa at residue 9 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 10, 16, 21, 22 and 24 may be Pro or hydroxy-Pro; Xaa at residues 17 and 25 may be Trp (D or L) or bromo-Trp (D or L)

<400> 165  
 Leu Val Ser His Thr Ser Ser Lys Xaa Xaa Gly Val Thr Phe Cys Xaa  
 1 5 10 15  
 Xaa Lys Val Cys Xaa Xaa Ala Xaa Xaa Arg Ile Leu Gly Val  
 20 25 30

<210> 166  
 <211> 619  
 <212> DNA  
 <213> *Conus nobilis*

<220>  
 <221> CDS  
 <222> (21)..(350)

<400> 166  
 gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg atg atg gtg 53  
 Met Gln Thr Ala Tyr Trp Val Met Met Met Val  
 1 5 10

gtg gtg atg atg gtg ggg gtt act gtc gct ggc tca ctg tct gtg ttt 101  
 Val Val Met Met Val Gly Val Thr Val Ala Gly Ser Leu Ser Val Phe  
 15 20 25

gat gat gac aac gac tct gac cca gct gtc aag cgc gcc atc acg tgg 149  
 Asp Asp Asp Asn Asp Ser Asp Pro Ala Val Lys Arg Ala Ile Thr Trp  
 30 35 40

tct cga ttc ctg ggc gcg tct cca gcc ttc ctg gca cag cag cga gcg 197  
 Ser Arg Phe Leu Gly Ala Ser Pro Ala Phe Leu Ala Gln Gln Arg Ala  
 45 50 55

ctg gct ccc ttc gcc aac cga ccc atc aat gag cag aaa cgt ttc cga 245  
 Leu Ala Pro Phe Ala Asn Arg Pro Ile Asn Glu Gln Lys Arg Phe Arg  
 60 65 70 75

cct gcc gtg aag agc cga tca cga cga gcg ccg ccg tgc gtg tgg aag 293  
 Pro Ala Val Lys Ser Arg Ser Arg Arg Ala Pro Pro Cys Val Trp Lys  
 80 85 90

gtg tgt ccc gct ccc ccc tgg ctg gtc acc aaa cgt aaa cag gaa acc 341  
 Val Cys Pro Ala Pro Pro Trp Leu Val Thr Lys Arg Lys Gln Glu Thr  
 95 100 105

agc gac tac tgacgtcata cctcaataga ccgactcatg acttcaacgc 390

Ser Asp Tyr  
110

tgaattgacg tcaccgagag ctccaacgtc acagcaggag cgagagagag agagagagag 450  
agagaaagag agagagaaag gctggagtat ttctctttct tttgggtttt cgtgttgaag 510  
tgtgatcagc tgggctgggt caaaattggt gaataaagtt gaatgaaaat caaaaaaaaa 570  
aaaaaaaaaa aagtactctg cgttggttact cgagcttaag ggcgaattc 619

<210> 167

<211> 110

<212> PRT

<213> Conus nobilis

<400> 167

Met Gln Thr Ala Tyr Trp Val Met Met Met Val Val Val Met Met Val  
1 5 10 15  
Gly Val Thr Val Ala Gly Ser Leu Ser Val Phe Asp Asp Asp Asn Asp  
20 25 30

Ser Asp Pro Ala Val Lys Arg Ala Ile Thr Trp Ser Arg Phe Leu Gly  
35 40 45

Ala Ser Pro Ala Phe Leu Ala Gln Gln Arg Ala Leu Ala Pro Phe Ala  
50 55 60

Asn Arg Pro Ile Asn Glu Gln Lys Arg Phe Arg Pro Ala Val Lys Ser  
65 70 75 80

Arg Ser Arg Arg Ala Pro Pro Cys Val Trp Lys Val Cys Pro Ala Pro  
85 90 95

Pro Trp Leu Val Thr Lys Arg Lys Gln Glu Thr Ser Asp Tyr  
100 105 110

<210> 168

<211> 37

<212> PRT

<213> Conus nobilis

<220>

<221> PEPTIDE

<222> (1)..(37)

<223> Xaa at residues 3, 13, 14, 21, 23 and 24 may be Pro or hydroxy-Pr  
o; Xaa at residues 17 and 25 may be Trp (D or L) or bromo-Trp (D  
or L); Xaa at residue 33 may be Glu or Gla;

<220>

<221> PEPTIDE

<222> (1)..(37)

<223> Xaa at residue 37 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Ty  
r, O-sulpho-Tyr or O-phospho-Tyr

<400> 168

Phe Arg Xaa Ala Val Lys Ser Arg Ser Arg Arg Ala Xaa Xaa Cys Val  
1 5 10 15

Xaa Lys Val Cys Xaa Ala Xaa Xaa Xaa Leu Val Thr Lys Arg Lys Gln

20 25 30  
 Xaa Thr Ser Asp Xaa  
 35  
 <210> 169  
 <211> 494  
 <212> DNA  
 <213> *Conus nobilis*  
 <220>  
 <221> CDS  
 <222> (21)..(242)  
 <400> 169  
 gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met  
 1 5 10  
 atg gtg tgg att aca gcc cct ctg tct gaa ggt ggt aaa ttg aac gac 101  
 Met Val Trp Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp  
 15 20 25  
 gta att cgg ggt ttg gtg cca cac ttc tta acc cca cag cat atc ttg 149  
 Val Ile Arg Gly Leu Val Pro His Phe Leu Thr Pro Gln His Ile Leu  
 30 35 40  
 caa agt ctg act tcc cgt aat ggt tct ggc agc agt aat cag aaa gaa 197  
 Gln Ser Leu Thr Ser Arg Asn Gly Ser Gly Ser Ser Asn Gln Lys Glu  
 45 50 55  
 gcg caa cta tgc atc tgg aag gta tgt cca cca acc cca tgg aga 242  
 Ala Gln Leu Cys Ile Trp Lys Val Cys Pro Pro Thr Pro Trp Arg  
 60 65 70  
 tgatcacaag gaaaaagatg aacggcgtca gacaaccgcc acaactgtag tgggacatcg 302  
 ttgatacgac ttcagcaa attttaacat cactgtggtt gtgaagaaat cagttgtttt 362  
 aaaagattgg atttttcctt gtttaagagt tgtactgata tcagctctgc actatgaaat 422  
 aaagctgatg tgacaagcaa aaaaaaaaaa aaaaagtact ctgcgttggt actcgagctt 482  
 aagggcgaat tc 494  
 <210> 170  
 <211> 74  
 <212> PRT  
 <213> *Conus nobilis*  
 <400> 170  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15  
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu  
 20 25 30  
 Val Pro His Phe Leu Thr Pro Gln His Ile Leu Gln Ser Leu Thr Ser  
 35 40 45

Arg Asn Gly Ser Gly Ser Ser Asn Gln Lys Glu Ala Gln Leu Cys Ile  
 50 55 60

Trp Lys Val Cys Pro Pro Thr Pro Trp Arg  
 65 70

<210> 171

<211> 25

<212> PRT

<213> Conus nobilis

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 10 may be Glu or Gla; Xaa at residues 16 and 24 may be Trp or bromo-Trp; Xaa at residues 20, 21 and 23 may be Pro or hydroxy-Pro

<400> 171

Asn Gly Ser Gly Ser Ser Asn Gln Lys Xaa Ala Gln Leu Cys Ile Xaa  
 1 5 10 15

Lys Val Cys Xaa Xaa Thr Xaa Xaa Arg  
 20 25

<210> 172

<211> 604

<212> DNA

<213> Conus nobilis

<220>

<221> CDS

<222> (21)..(350)

<400> 172

gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg atg atg gtg 53  
 Met Gln Thr Ala Tyr Trp Val Met Met Met Val  
 1 5 10

gtg gtg atg atg gtg ggg gtt act gtc gct ggc tca ctg tct gtg ttt 101  
 Val Val Met Met Val Gly Val Thr Val Ala Gly Ser Leu Ser Val Phe  
 15 20 25

gat gac gac aat gac tct gac cca gct gtc aag cgc gcc atc acg tgg 149  
 Asp Asp Asp Asn Asp Ser Asp Pro Ala Val Lys Arg Ala Ile Thr Trp  
 30 35 40

tct cga ttc ctg ggc gcg tct cca gcc ttc ctg gca cag cag cga gcg 197  
 Ser Arg Phe Leu Gly Ala Ser Pro Ala Phe Leu Ala Gln Gln Arg Ala  
 45 50 55

ctg gct ccc ttc gcc aac cga ccc atc aat gag cag aaa cgt ttc cga 245  
 Leu Ala Pro Phe Ala Asn Arg Pro Ile Asn Glu Gln Lys Arg Phe Arg  
 60 65 70 75

cct gcc gtg aag agc cga tca cga cga gcg ccg ccg tgc gta tgg aag 293  
 Pro Ala Val Lys Ser Arg Ser Arg Arg Ala Pro Pro Cys Val Trp Lys  
 80 85 90



gtg tgt ccc gct ccc ccc tgg ctg gtc acc aaa cgt aaa cag gaa acc 341  
 Val Cys Pro Ala Pro Pro Trp Leu Val Thr Lys Arg Lys Gln Glu Thr  
                   95                                  100                                  105

agc gac tac tgacgtcata cctcaataga ccgactcatg acttcaacgc 390  
 Ser Asp Tyr  
                   110

tgaattgacc tcaccgagag ctccaacgtc acagcaggag cgagagagag agagagagag 450

agagagagag aaaggctgga gtatttctct ttctttcggg ttttcgtggt gaagtgtgat 510

cagctgggct ggttcaaaat tgttgaataa agttgaataa aaaaaaaaaa aaaaaaagta 570

ctctgcgttg ttactcgagc ttaagggcga attc 604

<210> 173

<211> 110

<212> PRT

<213> Conus nobilis

<400> 173

Met Gln Thr Ala Tyr Trp Val Met Met Met Val Val Val Met Met Val  
 1                  5                                  10                                  15

Gly Val Thr Val Ala Gly Ser Leu Ser Val Phe Asp Asp Asp Asn Asp  
                   20                                  25                                  30

Ser Asp Pro Ala Val Lys Arg Ala Ile Thr Trp Ser Arg Phe Leu Gly  
                   35                                  40                                  45

Ala Ser Pro Ala Phe Leu Ala Gln Gln Arg Ala Leu Ala Pro Phe Ala  
                   50                                  55                                  60

Asn Arg Pro Ile Asn Glu Gln Lys Arg Phe Arg Pro Ala Val Lys Ser  
 65                                  70                                  75                                  80

Arg Ser Arg Arg Ala Pro Pro Cys Val Trp Lys Val Cys Pro Ala Pro  
                   85                                  90                                  95

Pro Trp Leu Val Thr Lys Arg Lys Gln Glu Thr Ser Asp Tyr  
                   100                                  105                                  110

<210> 174

<211> 37

<212> PRT

<213> Conus nobilis

<220>

<221> PEPTIDE

<222> (1)..(37)

<223> Xaa at residues 3, 13, 14, 21, 23 and 24 may be Pro or hydroxy-Pro;  
 o; Xaa at residues 17 and 25 may be Trp (D or L) or bromo-Trp (D  
 or L); Xaa at residue 33 may be Glu or Gla;

<220>

<221> PEPTIDE

<222> (1)..(37)

<223> Xaa at residue 37 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,  
 r, O-sulpho-Tyr or O-phospho-Tyr

&lt;400&gt; 174

Phe Arg Xaa Ala Val Lys Ser Arg Ser Arg Arg Ala Xaa Xaa Cys Val  
 1 5 10 15

Xaa Lys Val Cys Xaa Ala Xaa Xaa Xaa Leu Val Thr Lys Arg Lys Gln  
 20 25 30

Xaa Thr Ser Asp Xaa  
 35

&lt;210&gt; 175

&lt;211&gt; 391

&lt;212&gt; DNA

<213> *Conus parius*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (21)..(275)

&lt;400&gt; 175

gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met  
 1 5 10

atg gtg gtg tgg att aca gcc cct ttg tct gaa ggt ggt aaa ccg aag 101  
 Met Val Val Trp Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Pro Lys  
 15 20 25

cac gca att cgg ggt ttg gtg cca gac gac tta acc cca cag ctt atc 149  
 His Ala Ile Arg Gly Leu Val Pro Asp Asp Leu Thr Pro Gln Leu Ile  
 30 35 40

ttg cga agt ctg att tcc cgt cgt agt tct ttc ggc aag gat gcg aaa 197  
 Leu Arg Ser Leu Ile Ser Arg Arg Ser Ser Phe Gly Lys Asp Ala Lys  
 45 50 55

ccc ccc ttt agt tgt tca ggc ctc cga ggg ggt tgc gtc cta cct ccc 245  
 Pro Pro Phe Ser Cys Ser Gly Leu Arg Gly Gly Cys Val Leu Pro Pro  
 60 65 70 75

aat ctc agg cca aag ttc aac aaa ggt gga taacaaaccc aagcgttcct 295  
 Asn Leu Arg Pro Lys Phe Asn Lys Gly Gly  
 80 85

agttatacga atgccagcaa ataaaagcag tttgattgtg aaaaaaaaaa aaaaaaaaaag 355

tactctgcgt tgttactcga gcttaagggc gaattc 391

&lt;210&gt; 176

&lt;211&gt; 85

&lt;212&gt; PRT

<213> *Conus parius*

&lt;400&gt; 176

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Val Trp Ile  
 1 5 10 15

Thr Ala Pro Leu Ser Glu Gly Gly Lys Pro Lys His Ala Ile Arg Gly  
 20 25 30

Leu Val Pro Asp Asp Leu Thr Pro Gln Leu Ile Leu Arg Ser Leu Ile  
 35 40 45

Ser Arg Arg Ser Ser Phe Gly Lys Asp Ala Lys Pro Pro Phe Ser Cys  
 50 55 60

Ser Gly Leu Arg Gly Gly Cys Val Leu Pro Pro Asn Leu Arg Pro Lys  
 65 70 75 80

Phe Asn Lys Gly Gly  
 85

<210> 177

<211> 25

<212> PRT

<213> Conus parius

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residues 1, 3, 15, 16 and 20 may be Pro or hydroxy-Pro

<400> 177

Xaa Xaa Phe Ser Cys Ser Gly Leu Arg Gly Gly Cys Val Leu Xaa Xaa  
 1 5 10 15

Asn Leu Arg Xaa Lys Phe Asn Lys Gly  
 20 25

<210> 178

<211> 390

<212> DNA

<213> Conus parius

<220>

<221> CDS

<222> (19)..(273)

<400> 178

gaattcgccc ttggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 51  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met  
 1 5 10

atg gtg atg tgg att aca gcc cct ctg tct gaa ggt ggt aaa ccg aag 99  
 Met Val Met Trp Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Pro Lys  
 15 20 25

ctc ata att cgg ggt ttg gtg cca aac gac tta acc cca cag cgt atc 147  
 Leu Ile Ile Arg Gly Leu Val Pro Asn Asp Leu Thr Pro Gln Arg Ile  
 30 35 40

ttg cga agt ctg att tcc ggg cgt act tat ggc atc tat gat gcg aaa 195  
 Leu Arg Ser Leu Ile Ser Gly Arg Thr Tyr Gly Ile Tyr Asp Ala Lys  
 45 50 55

ccc ccc ttt agt tgt gca ggc ctc cga ggg ggt tgc gtc cta cct ccc 243  
 Pro Pro Phe Ser Cys Ala Gly Leu Arg Gly Gly Cys Val Leu Pro Pro  
 60 65 70 75

aat ctc agg cca aag ttc aag gaa ggt cga taaaaaaccc aagcggttcct 293  
 Asn Leu Arg Pro Lys Phe Lys Glu Gly Arg  
                   80                                  85

agttatacga atgccagcaa ataaaagcag ttgtattgcg aaaaaaaaaa aaaaaaaaaa 353  
 gtactctgcg ttgttactcg agcttaaggg cgaattc 390

<210> 179  
 <211> 85  
 <212> PRT  
 <213> Conus parius

<400> 179  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Met Trp Ile  
 1                  5                                  10                                  15  
 Thr Ala Pro Leu Ser Glu Gly Gly Lys Pro Lys Leu Ile Ile Arg Gly  
                   20                                  25                                  30  
 Leu Val Pro Asn Asp Leu Thr Pro Gln Arg Ile Leu Arg Ser Leu Ile  
                   35                                  40                                  45  
 Ser Gly Arg Thr Tyr Gly Ile Tyr Asp Ala Lys Pro Pro Phe Ser Cys  
           50                                  55                                  60  
 Ala Gly Leu Arg Gly Gly Cys Val Leu Pro Pro Asn Leu Arg Pro Lys  
 65                                  70                                  75                                  80  
 Phe Lys Glu Gly Arg  
                                   85

<210> 180  
 <211> 24  
 <212> PRT  
 <213> Conus parius

<220>  
 <221> PEPTIDE  
 <222> (1)..(24)  
 <223> Xaa at residues 1, 2, 15, 16 and 20 may be Pro or hydroxy-Pro; Xa  
       a at residue 24 may be Glu or Gla

<400> 180  
 Xaa Xaa Phe Ser Cys Ala Gly Leu Arg Gly Gly Cys Val Leu Xaa Xaa  
 1                  5                                  10                                  15  
 Asn Leu Arg Xaa Lys Phe Lys Xaa  
                   20

<210> 181  
 <211> 489  
 <212> DNA  
 <213> Conus planorbis

<220>  
 <221> CDS  
 <222> (21)..(251)

<400> 181  
 gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg atg atg atg 53

## 85

[illegible]

ue 21 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 183

Ser Ser Ser Asn Gly Leu Lys Arg Ala Asp Leu Cys Ile His Lys Ile  
1 5 10 15

Cys Xaa Xaa Arg Xaa His Gln Ser Gln Gln  
20 25

<210> 184

<211> 834

<212> DNA

<213> *Conus pulicarius*

<220>

<221> CDS

<222> (1)..(246)

<220>

<221> misc\_feature

<222> (1)..(834)

<223> n may be any nucleotide

<400> 184

atg cag acg gcc tac tgg gtg atg gtg atg atg atg atg gtg tgg gtt 48  
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Met Val Trp Val  
1 5 10 15

aca gcg cct gtg tct gaa ggt ggt aaa ttg agc gac gta att cgg ggt 96  
Thr Ala Pro Val Ser Glu Gly Gly Lys Leu Ser Asp Val Ile Arg Gly  
20 25 30

ttg gtg cca gac gac ata acc cca cag att att ttg caa agt ctg aat 144  
Leu Val Pro Asp Asp Ile Thr Pro Gln Ile Ile Leu Gln Ser Leu Asn  
35 40 45

gcc agt cgt cat gct tac aga cgt gtt cgt ctg aga gga cag ata tgt 192  
Ala Ser Arg His Ala Tyr Arg Arg Val Arg Leu Arg Gly Gln Ile Cys  
50 55 60

atc tgg aag gta tgt cca cca cta cta caa tgg ata cat cca tta gta 240  
Ile Trp Lys Val Cys Pro Pro Leu Leu Gln Trp Ile His Pro Leu Val  
65 70 75 80

aaa aga tgaatgacat cagacaaccg ccacaactgt agtacgacat cgттаacacg 296  
Lys Arg

acttcagcaa atattctaac atcacagtgg gttgtgaaga natcgggttg gctttaaaaa 356

aaanaatggg ggnttttccc cntgggttta aaaaaanntn ggnnccgggn aannncccn 416

nntnnncccc ccccnntngg gagaaaaaaa aaannccnnt nnnnggggggn nnncnaaaaa 476

aaaaaaaaa aaaaaaaaaa aaaaancccc nggggggngtg ntttnncccc cnccccngg 536

gggggggggn gnttttnccc ccccccgng gggggggggg ntttnnttt nngggggngc 596

cccccccccc cccnnnnnnn nnaanaannn nngggggggg ggaanaaaaa nannnnnnnn 656

nnnnnnnnnnn tttntcnnnt cnnccgngnn gnnaaaaaaa aaanttnatt tntnnannnc 716  
 nncnnnccnn cnnccncccc ncccccncc ncnncanncn nagannanga ggggggggng 776  
 nnnnggngna nnnnnannnn nnnngaannng agngngnnnn cncgncnncg cncnngnc 834

<210> 185  
 <211> 82  
 <212> PRT  
 <213> Conus pulicarius

<400> 185  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Met Val Trp Val  
 1 5 10 15  
 Thr Ala Pro Val Ser Glu Gly Gly Lys Leu Ser Asp Val Ile Arg Gly  
 20 25 30  
 Leu Val Pro Asp Asp Ile Thr Pro Gln Ile Ile Leu Gln Ser Leu Asn  
 35 40 45  
 Ala Ser Arg His Ala Tyr Arg Arg Val Arg Leu Arg Gly Gln Ile Cys  
 50 55 60  
 Ile Trp Lys Val Cys Pro Pro Leu Leu Gln Trp Ile His Pro Leu Val  
 65 70 75 80

Lys Arg

<210> 186  
 <211> 26  
 <212> PRT  
 <213> Conus pulicarius

<220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residues 10 and 19 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 14, 15 and 22 may be Pro or hydroxy-Pro

<400> 186  
 Val Arg Leu Arg Gly Gln Ile Cys Ile Xaa Lys Val Cys Xaa Xaa Leu  
 1 5 10 15  
 Leu Gln Xaa Ile His Xaa Leu Val Lys Arg  
 20 25

<210> 187  
 <211> 471  
 <212> DNA  
 <213> Conus pulicarius

<220>  
 <221> CDS  
 <222> (1)..(246)

<400> 187  
 atg cag acg gcc tac tgg gtg atg gtg atg atg atg atg gtg tgg gtt  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Met Val Trp Val

1	5	10	15	
aca gcg cct gtg tct gaa ggt ggt aaa ttg agc gac gta att cgg ggt				96
Thr Ala Pro Val Ser Glu Gly Gly Lys Leu Ser Asp Val Ile Arg Gly				
	20	25	30	
ttg gtg cca gac gac tta acc cca cag att atc ttg caa agt ctg aat				144
Leu Val Pro Asp Asp Leu Thr Pro Gln Ile Ile Leu Gln Ser Leu Asn				
	35	40	45	
gcc agt cgt cat gct tac aga cgt gtt cgt ccg aga gga cag ata tgt				192
Ala Ser Arg His Ala Tyr Arg Arg Val Arg Pro Arg Gly Gln Ile Cys				
	50	55	60	
atc tgg aag gta tgt cca cca cta cta caa tgg ata cat cca tta gta				240
Ile Trp Lys Val Cys Pro Pro Leu Leu Gln Trp Ile His Pro Leu Val				
65	70	75	80	
aaa aga tgaatgacat cagacaaccg ccacaactgt agtacggcat cgtaaacacg				296
Lys Arg				
acttcagcaa atattttaac atcacagtgg ttgtgaagaa atcggttgct ttaaaaaaag				356
attggggtttt tccttggttta agagttgtac tgatatcagt tctgcactat gaaataaagc				416
tgatgtgacg aacaaaaaaaa aaaaaaaaaa aaagtactct gcgttggttac tcgag				471
<210> 188				
<211> 82				
<212> PRT				
<213> Conus pulicarius				
<400> 188				
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Met Val Trp Val				
1	5	10	15	
Thr Ala Pro Val Ser Glu Gly Gly Lys Leu Ser Asp Val Ile Arg Gly				
	20	25	30	
Leu Val Pro Asp Asp Leu Thr Pro Gln Ile Ile Leu Gln Ser Leu Asn				
	35	40	45	
Ala Ser Arg His Ala Tyr Arg Arg Val Arg Pro Arg Gly Gln Ile Cys				
	50	55	60	
Ile Trp Lys Val Cys Pro Pro Leu Leu Gln Trp Ile His Pro Leu Val				
65	70	75	80	
Lys Arg				
<210> 189				
<211> 26				
<212> PRT				
<213> Conus pulicarius				
<220>				
<221> PEPTIDE				
<222> (1)..(26)				
<223> Xaa at residues 3, 14, 15 and 22 may be Pro or hydroxy-Pro; Xaa a				



t residues 10 and 19 may be Trp (D or L) or bromo-Trp (D or L)

<400> 189

Val Arg Xaa Arg Gly Gln Ile Cys Ile Xaa Lys Val Cys Xaa Xaa Leu  
1 5 10 15

Leu Gln Xaa Ile His Xaa Leu Val Lys Arg  
20 25

<210> 190

<211> 471

<212> DNA

<213> Conus pulicarius

<220>

<221> CDS

<222> (1)..(246)

<400> 190

atg cag acg gcc tac tgg gtg atg gtg atg atg atg atg gtg tgg gtt 48  
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Met Val Trp Val  
1 5 10 15

aca gcg cct gtg tct gaa ggt ggt aaa ttg agc gac gta att cgg ggt 96  
Thr Ala Pro Val Ser Glu Gly Gly Lys Leu Ser Asp Val Ile Arg Gly  
20 25 30

ttg gtg cca gac gac ata acc cca cag att atc ttg caa agt ctg aat 144  
Leu Val Pro Asp Asp Ile Thr Pro Gln Ile Ile Leu Gln Ser Leu Asn  
35 40 45

gcc agt cgt cat gct tac aga cct gtt cgt ctg aga gga cag ata tgt 192  
Ala Ser Arg His Ala Tyr Arg Pro Val Arg Leu Arg Gly Gln Ile Cys  
50 55 60

atc tgg aag gta tgt cca cca cta cta caa tgg ata cat cca tta gta 240  
Ile Trp Lys Val Cys Pro Pro Leu Leu Gln Trp Ile His Pro Leu Val  
65 70 75 80

aaa aga tgaatgacat cagacaaccg ccacaactgt agtacgacat cgттаacacg 296  
Lys Arg

acttcagcaa atattttaac atcacagtgg ttgtgaagaa atcggttgct ttaaaaaaag 356

attgggtttt tccttgttta agagttgtac tgatatcagt tctgcactat gaaataaagc 416

tgatgtgacg aacaaaaaaaa aaaaaaaaaa aaagtactct gcgttggttac tcgag 471

<210> 191

<211> 82

<212> PRT

<213> Conus pulicarius

<400> 191

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Met Val Trp Val  
1 5 10 15

Thr Ala Pro Val Ser Glu Gly Gly Lys Leu Ser Asp Val Ile Arg Gly  
20 25 30

Leu Val Pro Asp Asp Ile Thr Pro Gln Ile Ile Leu Gln Ser Leu Asn  
 35 40 45

Ala Ser Arg His Ala Tyr Arg Pro Val Arg Leu Arg Gly Gln Ile Cys  
 50 55 60

Ile Trp Lys Val Cys Pro Pro Leu Leu Gln Trp Ile His Pro Leu Val  
 65 70 75 80

Lys Arg

<210> 192

<211> 27

<212> PRT

<213> Conus pulicarius

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residues 1, 15, 16 and 23 may be Pro or hydroxy-Pro; Xaa at residues 11 and 20 may be Trp (D or L) or bromo-Trp (D or L)

<400> 192

Xaa Val Arg Leu Arg Gly Gln Ile Cys Ile Xaa Lys Val Cys Xaa Xaa  
 1 5 10 15

Leu Leu Gln Xaa Ile His Xaa Leu Val Lys Arg  
 20 25

<210> 193

<211> 375

<212> DNA

<213> Conus rattus

<220>

<221> CDS

<222> (1)..(282)

<400> 193

atg cag acg gcc tac tgg gtg atg gtg atg atg gtg gtg gtg ggg ttc 48  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Val Val Val Gly Phe  
 1 5 10 15

acc gtc ggg ggt cac gtc cat caa tct cac agt cct aca tcg cgc agc 96  
 Thr Val Gly Gly His Val His Gln Ser His Ser Pro Thr Ser Arg Ser  
 20 25 30

cat ggt gat gac tcc att cat gac aag acg att cat caa cat ctg ttt 144  
 His Gly Asp Asp Ser Ile His Asp Lys Thr Ile His Gln His Leu Phe  
 35 40 45

gcc cgt ctt cct ctg gag aac aac gac gac cat cgt tct gtg gat ctt 192  
 Ala Arg Leu Pro Leu Glu Asn Asn Asp Asp His Arg Ser Val Asp Leu  
 50 55 60

cct gca ggg acc agc gca ggc gac atg aaa cca caa cgc caa aga cgt 240  
 Pro Ala Gly Thr Ser Ala Gly Asp Met Lys Pro Gln Arg Gln Arg Arg  
 65 70 75 80

ctc tgc tgc atc ttt gcc att ctt tgg ttc tgt tgt ctc ggt 282

## 91

Leu Cys Cys Ile Phe Ala Ile Leu Trp Phe Cys Cys Leu Gly  
                   85                                  90

taacagtaca aattgcaatg cactggccga ttgaaagaac tgcaataaac ggaaaaaaaa 342

aaaaaaaaaa agtactctgc gttgttactc gag 375

<210> 194

<211> 94

<212> PRT

<213> Conus rattus

<400> 194

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Val Val Val Gly Phe  
   1                  5                                  10                                  15

Thr Val Gly Gly His Val His Gln Ser His Ser Pro Thr Ser Arg Ser  
                   20                                  25                                  30

His Gly Asp Asp Ser Ile His Asp Lys Thr Ile His Gln His Leu Phe  
                   35                                  40                                  45

Ala Arg Leu Pro Leu Glu Asn Asn Asp Asp His Arg Ser Val Asp Leu  
                   50                                  55                                  60

Pro Ala Gly Thr Ser Ala Gly Asp Met Lys Pro Gln Arg Gln Arg Arg  
   65                                  70                                  75                                  80

Leu Cys Cys Ile Phe Ala Ile Leu Trp Phe Cys Cys Leu Gly  
                   85                                  90

<210> 195

<211> 13

<212> PRT

<213> Conus rattus

<220>

<221> PEPTIDE

<222> (1)..(13)

<223> Xaa at residue 9 may be Trp (D or L) or bromo-Trp (D or L)

<400> 195

Leu Cys Cys Ile Phe Ala Ile Leu Xaa Phe Cys Cys Leu  
   1                  5                                  10

<210> 196

<211> 494

<212> DNA

<213> Conus striatus

<220>

<221> CDS

<222> (21)..(287)

<400> 196

gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53  
                                   Met Gln Thr Ala Tyr Trp Val Met Val Met Met  
                                   1                                  5                                  10

atg gtg tgg att aca gcc cct ctg tct gaa ggt ggt aaa ttg aac gac 101

Met Val Trp Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp  
15 20 25

gta att cgg ggt ttg gtg cca cac atc tta acc cca cag cat atc ttg 149  
Val Ile Arg Gly Leu Val Pro His Ile Leu Thr Pro Gln His Ile Leu  
30 35 40

caa agt ctg att tcc cct ctt cgt tct aac aac ggt cgt tcg agt gga 197  
Gln Ser Leu Ile Ser Pro Leu Arg Ser Asn Asn Gly Arg Ser Ser Gly  
45 50 55

gca caa ata tgc atc tgg aag gta tgt cca cca tcc cca tgg aga caa 245  
Ala Gln Ile Cys Ile Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Gln  
60 65 70 75

cca caa gaa atg atg aat gac atc aga caa ccg cca caa ctg 287  
Pro Gln Glu Met Met Asn Asp Ile Arg Gln Pro Pro Gln Leu  
80 85

tagtacgaca tcgttgatac gacttttagca aatatttttaa catcactgtg gttgtgaaga 347

aatcagttgc tttaaaagat tggatttttc cttgtttaag agttgtactg atatcagctc 407

tgcactatga aataaagctg atgtgacaaa caaaaaaaaaa aaaaaaaaaa gtactctgcg 467

ttgttactcg agcttaaggg cgaattc 494

&lt;210&gt; 197

&lt;211&gt; 89

&lt;212&gt; PRT

&lt;213&gt; Conus striatus

&lt;400&gt; 197

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
1 5 10 15

Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu  
20 25 30

Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Leu Ile Ser  
35 40 45

Pro Leu Arg Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Ile  
50 55 60

Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Gln Pro Gln Glu Met Met  
65 70 75 80

Asn Asp Ile Arg Gln Pro Pro Gln Leu  
85

&lt;210&gt; 198

&lt;211&gt; 38

&lt;212&gt; PRT

&lt;213&gt; Conus striatus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(38)

&lt;223&gt; Xaa at residues 14 and 22 may be Trp (D or L) or bromo-Trp (D or

L); Xaa at residues 18, 19, 21, 25, 35 and 36 may be Pro or hydroxy-Pro; Xaa at residue 27 may be Glu or Gla

<400> 198

Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Ile Xaa Lys Val  
1 5 10 15

Cys Xaa Xaa Ser Xaa Xaa Arg Gln Xaa Gln Xaa Met Met Asn Asp Ile  
20 25 30

Arg Gln Xaa Xaa Gln Leu  
35

<210> 199

<211> 412

<212> DNA

<213> *Conus striolatus*

<220>

<221> CDS

<222> (1)..(240)

<400> 199

atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48  
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
1 5 10 15

gac cct ctg tct gaa ggt ggt aaa ttg aac gac gta att cgg ggt ttg 96  
Asp Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu  
20 25 30

gtg cca cgc atc tta acc cca cag cat acc ttg cga agt ccg act tcc 144  
Val Pro Arg Ile Leu Thr Pro Gln His Thr Leu Arg Ser Pro Thr Ser  
35 40 45

ctt ctt cgt tct aac acc ggt ggt tcg agt gga gca caa ata tgc atc 192  
Leu Leu Arg Ser Asn Thr Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile  
50 55 60

tgg aag gta tgt cca cca tcc cca tgg aga cga tca caa gga aaa aga 240  
Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Ser Gln Gly Lys Arg  
65 70 75 80

tgaatgacgt cagacaagcg ccacaactgt agtacgacat cggttgatagc acttcagcaa 300

gtattttaaac atcactgtgg ttgtgaagaa atcagttgct ttaaaagatt ggatttttcc 360

ttgtttaaga gttgtactga tatcagctct gccctgtgaa ataaagctga tg 412

<210> 200

<211> 80

<212> PRT

<213> *Conus striolatus*

<400> 200

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
1 5 10 15

Asp Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu  
20 25 30

Val Pro Arg Ile Leu Thr Pro Gln His Thr Leu Arg Ser Pro Thr Ser  
35 40 45

Leu Leu Arg Ser Asn Thr Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile  
50 55 60

Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Arg Ser Gln Gly Lys Arg  
65 70 75 80

<210> 201

<211> 26

<212> PRT

<213> Conus striolatus

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residues 14 and 22 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 18, 19 and 21 may be Pro or hydroxy-Pro

<400> 201

Ser Asn Thr Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile Xaa Lys Val  
1 5 10 15

Cys Xaa Xaa Ser Xaa Xaa Arg Arg Ser Gln  
20 25

<210> 202

<211> 412

<212> DNA

<213> Conus striolatus

<220>

<221> CDS

<222> (1)..(240)

<400> 202

atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48  
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
1 5 10 15

gcc cct ctg tct gaa ggt ggt aaa ttg aac gac gta att cgg ggt ttg 96  
Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu  
20 25 30

gtg cca cac atc tta acc cca cag cat atc ttg caa agt ctg att tcc 144  
Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Leu Ile Ser  
35 40 45

cct ctt cgt tct aac aac ggt cgt tcg agt gga gca caa ata tgc atc 192  
Pro Leu Arg Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Ile  
50 55 60

tgg aag gta tgt cca cca tcc cca tgg aga cga tca caa gga aaa aga 240  
Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Arg Ser Gln Gly Lys Arg  
65 70 75 80

tgaatgacgt cagacaagcg ccacaactgt agtacgacat cggttgatacg acttcagcaa 300

gtatttttaac atcactgtgg ttgtgaagaa atcagttgct ttaaaagatt ggatttttcc 360

ttgtttaaga gttgtactga tatcagctct gcactgtgaa ataaagctga tg 412

<210> 203  
 <211> 80  
 <212> PRT  
 <213> Conus striolatus

<400> 203  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15  
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu  
 20 25 30  
 Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Leu Ile Ser  
 35 40 45  
 Pro Leu Arg Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Ile  
 50 55 60  
 Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Arg Ser Gln Gly Lys Arg  
 65 70 75 80

<210> 204  
 <211> 26  
 <212> PRT  
 <213> Conus striolatus  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residues 14 and 22 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 18, 19 and 21 may be Pro or hydroxy-Pro

<400> 204  
 Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Ile Xaa Lys Val  
 1 5 10 15  
 Cys Xaa Xaa Ser Xaa Xaa Arg Arg Ser Gln  
 20 25

<210> 205  
 <211> 497  
 <212> DNA  
 <213> Conus striolatus

<220>  
 <221> CDS  
 <222> (21)..(257)

<400> 205  
 gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met  
 1 5 10  
 atg gtg tgg att aaa gac cct ctg tct gaa ggt ggt aaa ttg aac gac 101  
 Met Val Trp Ile Lys Asp Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp  
 15 20 25  
 gta att cgg ggt ttg gtg cca cac atc tta acc cca cag cat atc ttg 149

Val Ile Arg Gly Leu Val Pro His Ile Leu Thr Pro Gln His Ile Leu  
30 35 40

caa agt ctg att tcc cct ctt cgt tct aac aac ggt cgt tcg agt gga 197  
Gln Ser Leu Ile Ser Pro Leu Arg Ser Asn Asn Gly Arg Ser Ser Gly  
45 50 55

gca caa ata tgc aac tgg aag gta tgt cca cca tcc cca tgg aga cga 245  
Ala Gln Ile Cys Asn Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Arg  
60 65 70 75

cca cga gga aaa tgatgaatga catcagacaa ccgccacaac tgtagtacga 297  
Pro Arg Gly Lys

cttcgttgat acgacttttag caaatatattt aacatcactg tggttgtgaa gaaatcagtt 357

gcttttaaag attggatttt tccttgttta agagttgtac tgatatcagc tctgcactat 417

gaaataaagc tgatgtgaca aacaaaaaaaa aaaaaaaaaa aaagtactct gcgttgttac 477

tcgagcttaa gggcgaattc 497

<210> 206  
<211> 79  
<212> PRT  
<213> Conus striolatus

<400> 206  
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Val Trp Ile Lys  
1 5 10 15

Asp Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu  
20 25 30

Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Leu Ile Ser  
35 40 45

Pro Leu Arg Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Asn  
50 55 60

Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Arg Pro Arg Gly Lys  
65 70 75

<210> 207  
<211> 26  
<212> PRT  
<213> Conus striolatus

<220>  
<221> PEPTIDE  
<222> (1)..(26)  
<223> Xaa at residues 14 and 22 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 18, 19, 21 and 25 may be Pro or hydroxy-Pro

<400> 207  
Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Asn Xaa Lys Val  
1 5 10 15

Cys Xaa Xaa Ser Xaa Xaa Arg Arg Xaa Arg  
20 25





Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Gln Pro Gln Glu Met Met  
65 70 75 80

Asn Asp Ile Arg Gln Pro Pro Gln Leu  
85

<210> 210

<211> 38

<212> PRT

<213> Conus striolatus

<220>

<221> PEPTIDE

<222> (1)..(38)

<223> Xaa at residues 14 and 22 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 18, 19, 21, 25, 35 and 36 may be Pro or hydroxy-Pro; Xaa at residue 27 may be Glu or Gla

<400> 210

Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Ile Xaa Lys Val  
1 5 10 15

Cys Xaa Xaa Ser Xaa Xaa Arg Gln Xaa Gln Xaa Met Met Asn Asp Ile  
20 25 30

Arg Gln Xaa Xaa Gln Leu  
35

<210> 211

<211> 413

<212> DNA

<213> Conus sulcatus

<220>

<221> CDS

<222> (1)..(234)

<400> 211

atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48  
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
1 5 10 15

gcc tct ctg tct gaa ggt ggt aaa ccg aac gac gtc att cgg ggt ttt 96  
Ala Ser Leu Ser Glu Gly Gly Lys Pro Asn Asp Val Ile Arg Gly Phe  
20 25 30

gtg cca gac gac tta acc cca cag ctt atc ttg cga agt ctg att tcc 144  
Val Pro Asp Asp Leu Thr Pro Gln Leu Ile Leu Arg Ser Leu Ile Ser  
35 40 45

cgt cgt cgt tct gac aag gat gtt ggg aag aga atg gaa tgt tac tgg 192  
Arg Arg Arg Ser Asp Lys Asp Val Gly Lys Arg Met Glu Cys Tyr Trp  
50 55 60

aag gca tgt aga ccc acg cta tcg aga cga cat gat ctt ggg 234  
Lys Ala Cys Arg Pro Thr Leu Ser Arg Arg His Asp Leu Gly  
65 70 75

taaaagatga atgacgtcag acaacagcca caactatagt atgacatcgt taatagact 294

tcagcaaata ttttaacatc actgtggttg tgaagaaatc agttgcttta aaagattgga 354

tttttcogtg ttttaagagtt gtactgatat cagctctgcc ctgtgaaata aagctgatg 413

<210> 212

<211> 78

<212> PRT

<213> Conus sulcatus

<400> 212

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
1 5 10 15

Ala Ser Leu Ser Glu Gly Gly Lys Pro Asn Asp Val Ile Arg Gly Phe  
20 25 30

Val Pro Asp Asp Leu Thr Pro Gln Leu Ile Leu Arg Ser Leu Ile Ser  
35 40 45

Arg Arg Arg Ser Asp Lys Asp Val Gly Lys Arg Met Glu Cys Tyr Trp  
50 55 60

Lys Ala Cys Arg Pro Thr Leu Ser Arg Arg His Asp Leu Gly  
65 70 75

<210> 213

<211> 27

<212> PRT

<213> Conus sulcatus

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 11 may be Glu or Gla; Xaa at residue 13 may be Tyr  
, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-  
-Tyr; Xaa at residue 14 may be Trp (D or L) or bromo-Trp (D or L)  
; Xaa at residue 19 may be Pro or hydroxy-Pro

<400> 213

Arg Ser Asp Lys Asp Val Gly Lys Arg Met Xaa Cys Xaa Xaa Lys Ala  
1 5 10 15

Cys Arg Xaa Thr Leu Ser Arg Arg His Asp Leu  
20 25

<210> 214

<211> 472

<212> DNA

<213> Conus terebra

<220>

<221> CDS

<222> (1)..(234)

<400> 214

atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48  
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
1 5 10 15

gcc cct ctg tct gaa ggt gat aaa ttg aac gac gta att cgg ggt ttg 96

Ala Pro Leu Ser Glu Gly Asp Lys Leu Asn Asp Val Ile Arg Gly Leu  
20 25 30

gtg cca gat aac tta gcc cca cag ctt gtt ttg caa agt ctg gat tcc 144  
Val Pro Asp Asn Leu Ala Pro Gln Leu Val Leu Gln Ser Leu Asp Ser  
35 40 45

cgt cgt cat cct cac ggc att cgt cag gat gga gcc caa ata tgt atc 192  
Arg Arg His Pro His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile  
50 55 60

tgg aag ata tgt cca cca tcc cca tgg aaa cga ctt gga tct 234  
Trp Lys Ile Cys Pro Pro Ser Pro Trp Lys Arg Leu Gly Ser  
65 70 75

taagaaaaga aacaattgac gtcagacaac cgccacaact tgagtacgac atcgttaata 294

caacttcagc aaatatgaaa ttttcagcat cactgtgggt gtgaagaaat cagttgcttt 354

aaaagattgg atttgcctt gtttaagagt tgtactgatg tcattctctgc actgtgaaat 414

aaagctgatg tgacaaacaa aaaaaaaaaa aaaaaagtac tctgcgttgt tactcgag 472

<210> 215  
<211> 78  
<212> PRT  
<213> Conus terebra

<400> 215  
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
1 5 10 15

Ala Pro Leu Ser Glu Gly Asp Lys Leu Asn Asp Val Ile Arg Gly Leu  
20 25 30

Val Pro Asp Asn Leu Ala Pro Gln Leu Val Leu Gln Ser Leu Asp Ser  
35 40 45

Arg Arg His Pro His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile  
50 55 60

Trp Lys Ile Cys Pro Pro Ser Pro Trp Lys Arg Leu Gly Ser  
65 70 75

<210> 216  
<211> 28  
<212> PRT  
<213> Conus terebra

<220>  
<221> PEPTIDE  
<222> (1)..(28)  
<223> Xaa at residues 2, 19, 20 and 22 may be Pro or hydroxy-Pro; Xaa a  
t residues 15 and 23 may be Trp (D or L) or bromo-Trp (D or L)

<400> 216  
His Xaa His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile Xaa Lys  
1 5 10 15

Ile Cys Xaa Xaa Ser Xaa Xaa Lys Arg Leu Gly Ser

20

25

<210> 217  
 <211> 474  
 <212> DNA  
 <213> *Conus terebra*

<220>  
 <221> CDS  
 <222> (1)..(234)

<400> 217  
 atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15  
 gcc cct ctg tct gaa ggt gat aaa ttg aac gac gta att cgg ggt ttg 96  
 Ala Pro Leu Ser Glu Gly Asp Lys Leu Asn Asp Val Ile Arg Gly Leu  
 20 25 30  
 gtg cca gat aac tta gcc cca cag ctt gtt ttg cat agt ctg gat tcc 144  
 Val Pro Asp Asn Leu Ala Pro Gln Leu Val Leu His Ser Leu Asp Ser  
 35 40 45  
 cgt cgt cat cct cac ggc att cgt cag gat gga gcc caa ata tgt atc 192  
 Arg Arg His Pro His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile  
 50 55 60  
 tgg aag ata tgt cca cca tcc cca tgg aga cga ctt gga tct 234  
 Trp Lys Ile Cys Pro Pro Ser Pro Trp Arg Arg Leu Gly Ser  
 65 70 75  
 taagaaaaga aacaattgac gtcagacaac cgccacatct tgagtacgac atcgттаааа 294  
 cgacttcagc aaatatgaaa ttttcagcat cactgtgggt gtgaagaaat cagttgcctt 354  
 aaaagattgg atttgcctt gtttaagagt tgtactgatg tcattctctgc actatgaaat 414  
 aaagctgatg tgacaaacaa aaaaaaaaaa aaaaaaaagt actctgcggt gttactcgag 474

<210> 218  
 <211> 78  
 <212> PRT  
 <213> *Conus terebra*

<400> 218  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15  
 Ala Pro Leu Ser Glu Gly Asp Lys Leu Asn Asp Val Ile Arg Gly Leu  
 20 25 30  
 Val Pro Asp Asn Leu Ala Pro Gln Leu Val Leu His Ser Leu Asp Ser  
 35 40 45  
 Arg Arg His Pro His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile  
 50 55 60  
 Trp Lys Ile Cys Pro Pro Ser Pro Trp Arg Arg Leu Gly Ser  
 65 70 75

<210> 219  
 <211> 28  
 <212> PRT  
 <213> *Conus terebra*

<220>  
 <221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residues 2, 19, 20 and 22 may be Pro or hydroxy-Pro; Xaa at residues 15 and 23 may be Trp (D or L) or bromo-Trp (D or L)

<400> 219  
 His Xaa His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile Xaa Lys  
 1 5 10 15  
 Ile Cys Xaa Xaa Ser Xaa Xaa Arg Arg Leu Gly Ser  
 20 25

<210> 220  
 <211> 485  
 <212> DNA  
 <213> *Conus vexillum*

<220>  
 <221> CDS  
 <222> (21)..(236)

<400> 220  
 gaattcgccc ttatggatcc atg cag atg gcc tac tgg gtg atg gtg atg atg 53  
 Met Gln Met Ala Tyr Trp Val Met Val Met Met  
 1 5 10  
 atg gtg tgg att aaa ggc cct gtg tcc gaa ggt ggt aaa ttg aac gac 101  
 Met Val Trp Ile Lys Gly Pro Val Ser Glu Gly Gly Lys Leu Asn Asp  
 15 20 25  
 gta att cgg ggt ttg gtg cca gac gac ttg acc cca gtg tct gcc ttg 149  
 Val Ile Arg Gly Leu Val Pro Asp Asp Leu Thr Pro Val Ser Ala Leu  
 30 35 40  
 cat cat ccg gtt tcc cat cgt cgg tct cac agc agt agt ttg tgg tgt 197  
 His His Pro Val Ser His Arg Arg Ser His Ser Ser Ser Leu Trp Cys  
 45 50 55  
 gta tgt cca ttc agg gtg tgt cca cca tgc cat gga aga tgacctggtc 246  
 Val Cys Pro Phe Arg Val Cys Pro Pro Cys His Gly Arg  
 60 65 70  
 ccaaaccaac aaaataacgt cagacaaccg ccacaacttt agtacgacat cccttaatac 306  
 gacttcagca agtatttttaa catcactatg gtgtgatgaa atcagttgct ttaaaagatt 366  
 ggattttttcc ttgtttaaga gttgcactga taacagccca gcagtatgaa ataaagttga 426  
 tgtggcaaaa aaaaaaaaaa aagtactctg cggtgttact cgagcttaag ggccaattc 485

<210> 221  
 <211> 72  
 <212> PRT

<213> Conus vexillum

<400> 221

Met Gln Met Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Lys  
1 5 10 15

Gly Pro Val Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu  
20 25 30

Val Pro Asp Asp Leu Thr Pro Val Ser Ala Leu His His Pro Val Ser  
35 40 45

His Arg Arg Ser His Ser Ser Ser Leu Trp Cys Val Cys Pro Phe Arg  
50 55 60

Val Cys Pro Pro Cys His Gly Arg  
65 70

<210> 222

<211> 19

<212> PRT

<213> Conus vexillum

<220>

<221> PEPTIDE

<222> (1)..(19)

<223> Xaa at residue 7 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 11, 16 and 17 may be Pro or hydroxy-Pro

<400> 222

Ser His Ser Ser Ser Leu Xaa Cys Val Cys Xaa Phe Arg Val Cys Xaa  
1 5 10 15

Xaa Cys His

<210> 223

<211> 481

<212> DNA

<213> Conus vexillum

<220>

<221> CDS

<222> (21)..(257)

<400> 223

gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53  
Met Gln Thr Ala Tyr Trp Val Met Val Met Met  
1 5 10

atg gtg tgg att aca gcc cct ttg tct gaa ggt ggt aaa ctg aac gat 101  
Met Val Trp Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp  
15 20 25

gta att cgg ggt ttc gcg cta gat gac tta gcc caa agc cgt att atg 149  
Val Ile Arg Gly Phe Ala Leu Asp Asp Leu Ala Gln Ser Arg Ile Met  
30 35 40

caa agt ctg gtt ttc agt cat cag cct ctt cca acg gca tcc ata tgt 197  
Gln Ser Leu Val Phe Ser His Gln Pro Leu Pro Thr Ala Ser Ile Cys  
45 50 55

atc tgg aag ata tgt cca cca gac cca tgg aga cga cat gat ctt cag 245  
 Ile Trp Lys Ile Cys Pro Pro Asp Pro Trp Arg Arg His Asp Leu Gln  
 60 65 70 75

aaa agt aac aaa tgacgtcaga caaccgccac aacttgaata caacatcatt 297  
 Lys Ser Asn Lys

aatacgactt cagcaaatat tttagcatca ctgtgattgt tcggaagtca gttgctttaa 357

aagattggat ttgtccctgt tgtattgatg tcaactctgc actatgaaat aaagctgatg 417

tgacaagcaa aaaaaaaaaa aaaaaaagta ctctgcgttg ttactcgagc ttaagggcga 477

attc 481

<210> 224

<211> 79

<212> PRT

<213> Conus vexillum

<400> 224

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr  
 1 5 10 15

Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Phe  
 20 25 30

Ala Leu Asp Asp Leu Ala Gln Ser Arg Ile Met Gln Ser Leu Val Phe  
 35 40 45

Ser His Gln Pro Leu Pro Thr Ala Ser Ile Cys Ile Trp Lys Ile Cys  
 50 55 60

Pro Pro Asp Pro Trp Arg Arg His Asp Leu Gln Lys Ser Asn Lys  
 65 70 75

<210> 225

<211> 38

<212> PRT

<213> Conus vexillum

<220>

<221> PEPTIDE

<222> (1)..(38)

<223> Xaa at residues 11, 14, 24, 25 and 27 may be Pro or hydroxy-Pro;  
 Xaa at residues 20 and 28 may be Trp (D or L) or bromo-Trp (D or L)

<400> 225

Ile Met Gln Ser Leu Val Phe Ser His Gln Xaa Leu Xaa Thr Ala Ser  
 1 5 10 15

Ile Cys Ile Xaa Lys Ile Cys Xaa Xaa Asp Xaa Xaa Arg Arg His Asp  
 20 25 30

Leu Gln Lys Ser Asn Lys  
 35



<210> 226  
 <211> 384  
 <212> DNA  
 <213> Conus vexillum

<220>  
 <221> CDS  
 <222> (1)..(285)

<400> 226  
 atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg gtg ggg ttc 48  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Val Gly Phe  
 1 5 10 15  
 acc gtc gag agt cac gtc cat cag tct cac agt cct aca tcg cgc agc 96  
 Thr Val Glu Ser His Val His Gln Ser His Ser Pro Thr Ser Arg Ser  
 20 25 30  
 cat ggt gat gac tcc att cat gac aag acg att cat caa cat ctg ttt 144  
 His Gly Asp Asp Ser Ile His Asp Lys Thr Ile His Gln His Leu Phe  
 35 40 45  
 gcc cgt ctt cct ctg gag aac aac gac gac cat cgt tct gtg gat ctt 192  
 Ala Arg Leu Pro Leu Glu Asn Asn Asp Asp His Arg Ser Val Asp Leu  
 50 55 60  
 cct gca ggg act agc gca ggc gac atg aaa cca caa cgc cag aaa cgt 240  
 Pro Ala Gly Thr Ser Ala Gly Asp Met Lys Pro Gln Arg Gln Lys Arg  
 65 70 75 80  
 ttc tgc tgc atc ttt gcc ccg att ctt ttg ttc tgt tgt ttc ggt 285  
 Phe Cys Cys Ile Phe Ala Pro Ile Leu Leu Phe Cys Cys Phe Gly  
 85 90 95  
 taacagcaca aattacactg cactggccga ttgaaagaac tgcaataaac ggtaaagcaa 345  
 aaaaaaaaaa aaaaaaagta ctctgcgttg ttactcgag 384

<210> 227  
 <211> 95  
 <212> PRT  
 <213> Conus vexillum

<400> 227  
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Val Gly Phe  
 1 5 10 15  
 Thr Val Glu Ser His Val His Gln Ser His Ser Pro Thr Ser Arg Ser  
 20 25 30  
 His Gly Asp Asp Ser Ile His Asp Lys Thr Ile His Gln His Leu Phe  
 35 40 45  
 Ala Arg Leu Pro Leu Glu Asn Asn Asp Asp His Arg Ser Val Asp Leu  
 50 55 60  
 Pro Ala Gly Thr Ser Ala Gly Asp Met Lys Pro Gln Arg Gln Lys Arg  
 65 70 75 80  
 Phe Cys Cys Ile Phe Ala Pro Ile Leu Leu Phe Cys Cys Phe Gly  
 85 90 95

<210> 228  
 <211> 14  
 <212> PRT  
 <213> Conus vexillum

<220>  
 <221> PEPTIDE  
 <222> (1)..(14)  
 <223> Xaa at residue 7 may be Pro or hydroxy-Pro

<400> 228  
 Phe Cys Cys Ile Phe Ala Xaa Ile Leu Leu Phe Cys Cys Phe  
 1 5 10

<210> 229  
 <211> 40  
 <212> PRT  
 <213> Conus tulipa

<400> 229  
 Glx Thr Asp Val Leu Leu Glu Ala Thr Leu Leu Thr Thr Pro Ala Pro  
 1 5 10 15

Glu Gln Arg Leu Phe Cys Phe Trp Lys Ser Cys Trp Pro Arg Pro Tyr  
 20 25 30

Pro Trp Arg Arg Arg Asp Leu Asn  
 35 40

<210> 230  
 <211> 40  
 <212> PRT  
 <213> Conus magus

<400> 230  
 Glx Thr Asp Val Leu Leu Asp Ala Thr Leu Leu Thr Thr Pro Ala Pro  
 1 5 10 15

Glu Gln Arg Leu Phe Cys Phe Trp Lys Ser Cys Trp Pro Arg Pro Tyr  
 20 25 30

Pro Trp Arg Arg Arg Asn Leu Asn  
 35 40

<210> 231  
 <211> 40  
 <212> PRT  
 <213> Conus geographus

<400> 231  
 Glx Thr Asp Val Leu Leu Glu Ala Thr Leu Leu Thr Thr Pro Ala Pro  
 1 5 10 15

Glu Gln Arg Leu Phe Cys Phe Trp Lys Ser Cys Thr Trp Arg Pro Tyr  
 20 25 30

Pro Trp Arg Arg Arg Asp Leu Asn  
 35 40

<210> 232  
 <211> 21  
 <212> PRT  
 <213> *Conus tulipa*

<400> 232  
 Leu Phe Cys Phe Trp Lys Ser Cys Trp Pro Arg Pro Tyr Pro Trp Arg  
 1 5 10 15  
 Arg Arg Asp Leu Asn  
 20

<210> 233  
 <211> 21  
 <212> PRT  
 <213> *Conus magus*

<400> 233  
 Leu Phe Cys Phe Trp Lys Ser Cys Trp Pro Arg Pro Tyr Pro Trp Arg  
 1 5 10 15  
 Arg Arg Asn Leu Asn  
 20

<210> 234  
 <211> 21  
 <212> PRT  
 <213> *Conus geographus*

<400> 234  
 Leu Phe Cys Phe Trp Lys Ser Cys Thr Trp Arg Pro Tyr Pro Trp Arg  
 1 5 10 15  
 Arg Arg Asp Leu Asn  
 20

<210> 235  
 <211> 19  
 <212> PRT  
 <213> *Conus generalis*

<400> 235  
 Ser His Ser Ser Ser Leu Trp Cys Val Cys Pro Phe Arg Val Cys Pro  
 1 5 10 15  
 Pro Cys His

<210> 236  
 <211> 19  
 <212> PRT  
 <213> *Conus vexillum*

<400> 236  
 Ser His Ser Ser Ser Leu Trp Cys Val Cys Pro Phe Arg Val Cys Pro  
 1 5 10 15  
 Pro Cys His

<210> 237

<211> 33  
 <212> PRT  
 <213> *Conus flavidus*

<400> 237  
 His Asp His Gly Ile Arg Pro Lys Arg Val Asp Ile Cys Asn Trp Arg  
 1 5 10 15  
 Ile Cys Ala Pro Asn Pro Leu Arg Arg His Asp Leu Lys Lys Gly Asn  
 20 25 30

Asn

<210> 238  
 <211> 33  
 <212> PRT  
 <213> *Conus emaciatus*

<400> 238  
 His Thr His Gly Ile Arg Pro Lys Gly Asp Gly Ile Cys Ile Trp Lys  
 1 5 10 15  
 Val Cys Pro Pro Asp Pro Trp Arg Arg His Arg Leu Lys Lys Arg Asn  
 20 25 30

Asn

<210> 239  
 <211> 33  
 <212> PRT  
 <213> *Conus aurisiacus*

<400> 239  
 His Thr His Gly Ile Arg Pro Lys Gly Asp Gly Ile Cys Ile Trp Lys  
 1 5 10 15  
 Val Cys Pro Pro Asp Pro Trp Arg Arg His His Leu Lys Lys Arg Asn  
 20 25 30

Asn

<210> 240  
 <211> 28  
 <212> PRT  
 <213> *Conus terebra*

<400> 240  
 His Pro His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile Trp Lys  
 1 5 10 15  
 Ile Cys Pro Pro Ser Pro Trp Lys Arg Leu Gly Ser  
 20 25

<210> 241  
 <211> 28  
 <212> PRT  
 <213> *Conus terebra*

<400> 241  
 His Pro His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile Trp Lys  
 1 5 10 15

Ile Cys Pro Pro Ser Pro Trp Arg Arg Leu Gly Ser  
                   20                  25

<210> 242  
 <211> 28  
 <212> PRT  
 <213> Conus litoglyphus

<400> 242  
 His Pro His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile Trp Lys  
 1                  5                  10                  15

Ile Cys Pro Pro Ser Pro Trp Lys Arg Leu Gly Ser  
                   20                  25

<210> 243  
 <211> 28  
 <212> PRT  
 <213> Conus litoglyphus

<400> 243  
 His Pro His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile Trp Lys  
 1                  5                  10                  15

Ile Cys Pro Pro Ser Pro Trp Arg Arg Leu Gly Ser  
                   20                  25

<210> 244  
 <211> 23  
 <212> PRT  
 <213> Conus consors

<400> 244  
 Asp Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile Trp  
 1                  5                  10                  15

Lys Val Cys Pro Pro Ser Pro  
                   20

<210> 245  
 <211> 25  
 <212> PRT  
 <213> Conus consors

<400> 245  
 Asp Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile Trp  
 1                  5                  10                  15

Lys Val Cys Pro Pro Ser Pro Trp Lys  
                   20                  25

<210> 246  
 <211> 28  
 <212> PRT  
 <213> Conus consors

<400> 246  
 Ala Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile Trp  
 1                  5                  10                  15

Lys Val Cys Pro Pro Ser Pro Trp Arg Arg Pro Gln  
                   20                                  25

<210> 247  
 <211> 26  
 <212> PRT  
 <213> Conus striolatus

<400> 247  
 Ser Asn Thr Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile Trp Lys Val  
 1                  5                                  10                                  15

Cys Pro Pro Ser Pro Trp Arg Arg Ser Gln  
                   20                                  25

<210> 248  
 <211> 26  
 <212> PRT  
 <213> Conus striolatus

<400> 248  
 Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Asn Trp Lys Val  
 1                  5                                  10                                  15

Cys Pro Pro Ser Pro Trp Arg Arg Pro Arg  
                   20                                  25

<210> 249  
 <211> 26  
 <212> PRT  
 <213> Conus striolatus

<400> 249  
 Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Ile Trp Lys Val  
 1                  5                                  10                                  15

Cys Pro Pro Ser Pro Trp Arg Arg Ser Gln  
                   20                                  25

<210> 250  
 <211> 38  
 <212> PRT  
 <213> Conus striolatus

<400> 250  
 Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Ile Trp Lys Val  
 1                  5                                  10                                  15

Cys Pro Pro Ser Pro Trp Arg Gln Pro Gln Glu Met Met Asn Asp Ile  
                   20                                  25                                  30  
 Arg Gln Pro Pro Gln Leu  
                   35

<210> 251  
 <211> 38  
 <212> PRT  
 <213> Conus striatus

<400> 251

Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Ile Trp Lys Val  
 1 5 10 15

Cys Pro Pro Ser Pro Trp Arg Gln Pro Gln Glu Met Met Asn Asp Ile  
 20 25 30

Arg Gln Pro Pro Gln Leu  
 35

<210> 252

<211> 25

<212> PRT

<213> Conus aurisiacus

<400> 252

Leu His Ser Asp Ser Ser Asp Gln Lys Gly Ala Gln Ile Cys Ile Trp  
 1 5 10 15

Lys Val Cys Pro Pro Pro Pro Trp Arg  
 20 25

<210> 253

<211> 34

<212> PRT

<213> Conus aurisiacus

<400> 253

Leu His Ser Asp Ser Ser Asp Gln Lys Gly Gly Met Asn Ala Trp Thr  
 1 5 10 15

Gly Ala Gly Ala Gln Ile Cys Ile Trp Lys Val Cys Pro Pro Pro Pro  
 20 25 30

Trp Arg

<210> 254

<211> 37

<212> PRT

<213> Conus aurisiacus

<400> 254

Leu Arg Ser Asp Ser Ser Asp Gln Lys Gly Gly Met Asn Ala Ser Thr  
 1 5 10 15

Gly Ala Gly Ala Gln Ile Cys Ile Trp Lys Val Cys Pro Pro Ser Pro  
 20 25 30

Trp Arg Arg Thr Gln  
 35

<210> 255

<211> 28

<212> PRT

<213> Conus circumciscus

<400> 255

Leu Arg Ser Asp Ser Ser Gly Gln Lys Gly Ala Gln Ile Cys Ile Trp  
 1 5 10 15

Lys Val Cys Pro Leu Ser Pro Trp Arg Arg Pro Gln

20

25

&lt;210&gt; 256

&lt;211&gt; 32

&lt;212&gt; PRT

<213> *Conus circumcissus*

&lt;400&gt; 256

Leu	Arg	Ser	Asp	Ser	Ser	Gly	Gln	Lys	Gly	Ala	Gln	Ile	Cys	Ile	Trp
1				5					10					15	

Lys	Val	Cys	Pro	Leu	Ser	Pro	Trp	Arg	Arg	Pro	Gln	Gly	Lys	Asp	Glu
			20					25					30		

&lt;210&gt; 257

&lt;211&gt; 28

&lt;212&gt; PRT

<213> *Conus achatinus*

&lt;400&gt; 257

Leu	Arg	Ser	Asp	Asn	Gly	Gly	Ser	Ser	Gly	Ala	Gln	Ile	Cys	Ile	Trp
1				5					10					15	

Lys	Val	Cys	Pro	Pro	Ser	Pro	Trp	Arg	Arg	Pro	Gln
			20					25			

&lt;210&gt; 258

&lt;211&gt; 22

&lt;212&gt; PRT

<213> *Conus stercusmuscarum*

&lt;400&gt; 258

Leu	Gly	Ile	Gly	Ser	Ser	Asp	Gln	Asn	Ala	Gln	Ile	Cys	Ile	Trp	Lys
1				5					10					15	

Val	Cys	Pro	Pro	Ser	Pro
			20		

&lt;210&gt; 259

&lt;211&gt; 25

&lt;212&gt; PRT

<213> *Conus consors*

&lt;400&gt; 259

Asn	Gly	Ser	Gly	Ser	Ser	Asn	Gln	Lys	Glu	Ala	Gln	Leu	Cys	Ile	Trp
1				5					10					15	

Lys	Val	Cys	Pro	Pro	Ser	Pro	Trp	Arg
			20					25

&lt;210&gt; 260

&lt;211&gt; 25

&lt;212&gt; PRT

<213> *Conus consors*

&lt;400&gt; 260

Asn	Gly	Ser	Gly	Ser	Ser	Asn	Gln	Lys	Glu	Ala	Gln	Leu	Cys	Ile	Trp
1				5					10					15	

Lys	Val	Cys	Pro	Pro	Thr	Pro	Trp	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----



20

25

&lt;210&gt; 261

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Conus magus

&lt;400&gt; 261

Asn Gly Ser Gly Ser Ser Asn Gln Lys Glu Ala Gln Leu Cys Ile Trp  
 1 5 10 15

Lys Val Cys Pro Pro Ser Pro Trp Arg  
 20 25

&lt;210&gt; 262

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Conus nobilis

&lt;400&gt; 262

Asn Gly Ser Gly Ser Ser Asn Gln Lys Glu Ala Gln Leu Cys Ile Trp  
 1 5 10 15

Lys Val Cys Pro Pro Thr Pro Trp Arg  
 20 25

&lt;210&gt; 263

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Conus sulcatus

&lt;400&gt; 263

Arg Ser Asp Lys Asp Val Gly Lys Arg Met Glu Cys Tyr Trp Lys Ala  
 1 5 10 15

Cys Arg Pro Thr Leu Ser Arg Arg His Asp Leu  
 20 25

&lt;210&gt; 264

&lt;211&gt; 40

&lt;212&gt; PRT

&lt;213&gt; Conus bocki

&lt;400&gt; 264

Arg Ser Asp Lys Asp Asp Pro Gly Gly Gln Glu Cys Tyr Trp Asn Val  
 1 5 10 15

Cys Ala Pro Asn Gln Gly Asp His Met Ile Leu Arg Lys Lys Met Asn  
 20 25 30

Asp Asp Arg Gln Pro Pro Gln Leu  
 35 40

&lt;210&gt; 265

&lt;211&gt; 19

&lt;212&gt; PRT

&lt;213&gt; Conus betulinus

&lt;400&gt; 265

Arg Ser Asp Ser Asp Val Arg Glu Val Pro Val Cys Ser Trp Lys Ile

1	5	10	15
---	---	----	----

Cys Pro Pro

<210> 266

<211> 22

<212> PRT

<213> Conus loroisii

<400> 266

Arg Ser Asp Ser Asp Val Arg Glu Val Tyr Ile Leu Cys Ile Trp Lys  
1 5 10 15

Ile Cys Pro Pro Leu Pro  
20

<210> 267

<211> 32

<212> PRT

<213> Conus gladiator

<400> 267

His Pro Ala Asn Val Arg Gln Gln Gly Lys Ile Cys Val Trp Lys Val  
1 5 10 15

Cys Pro Pro Trp Pro Val Arg Ser Pro Gly Pro Gln Pro Lys Asn Lys  
20 25 30

<210> 268

<211> 32

<212> PRT

<213> Conus gladiator

<400> 268

His Pro Ala Asn Val Arg Gln Gln Gly Lys Ile Cys Val Trp Lys Val  
1 5 10 15

Cys Pro Pro Ser Pro Val Arg Ser Pro Gly Pro Leu Pro Lys Asn Lys  
20 25 30

<210> 269

<211> 41

<212> PRT

<213> Conus musicus

<400> 269

Gly Met Gly Pro Gly Asp Leu Ser Leu Gln Lys Met Phe Pro Ser Leu  
1 5 10 15

Ala Leu Gly Pro Gly Gly Asp Val Ile Cys Arg Trp Lys Val Cys Pro  
20 25 30

Pro Thr Pro Trp Lys Arg Leu Ile Lys  
35 40

 $\langle 210 \rangle$  270

<211> 49

&lt;212&gt; PRT

<213> Conus musicus

<400> 270  
 Gly Met Val Pro Gly Asp Leu Ala Leu Gln Tyr Leu Phe Pro Ser Leu  
 1 5 10 15

Ala Phe Asn Pro Pro Asp Ile Cys Thr Trp Lys Val Cys Pro Pro Pro  
 20 25 30

Pro Trp Arg Arg Pro Lys Lys Ile Thr Asp Val Gly Gln Pro Pro Gln  
 35 40 45

Leu

<210> 271

<211> 49

<212> PRT

<213> Conus musicus

<400> 271

Gly Met Val Pro Gly Asp Leu Val Leu Gln Tyr Leu Phe Pro Ser Leu  
 1 5 10 15

Ala Phe Ser Pro Pro Asp Ile Cys Thr Trp Lys Val Cys Pro Pro Pro  
 20 25 30

Pro Trp Arg Arg Pro Lys Lys Ile Thr Asp Val Arg Gln Pro Pro Gln  
 35 40 45

Leu

<210> 272

<211> 49

<212> PRT

<213> Conus musicus

<400> 272

Gly Met Val Pro Gly Asp Leu Val Leu Gln Tyr Leu Phe Pro Ser Leu  
 1 5 10 15

Ala Phe Asn Pro Pro Asp Ile Cys Thr Trp Lys Val Cys Pro Pro Pro  
 20 25 30

Pro Trp Arg Arg Pro Lys Lys Ile Thr Asp Val Arg Gln Pro Pro Gln  
 35 40 45

Leu

<210> 273

<211> 29

<212> PRT

<213> Conus miles

<400> 273

Glx Gln Asp Gln Ser Pro His His Val Cys Cys Ala Ile Gly Pro Val  
 1 5 10 15

Leu Pro Phe Cys Cys Val Ser Trp Leu His Lys Leu His  
 20 25

<210> 274

<211> 14

<212> PRT  
 <213> Conus miles

<400> 274  
 Leu Cys Cys Ile Phe Ala Pro Ile Leu Trp Phe Cys Cys His  
 1 5 10

<210> 275  
 <211> 13  
 <212> PRT  
 <213> Conus rattus

<400> 275  
 Leu Cys Cys Ile Phe Ala Ile Leu Trp Phe Cys Cys Leu  
 1 5 10

<210> 276  
 <211> 15  
 <212> PRT  
 <213> Conus capitaneus

<400> 276  
 Gly Phe Cys Cys Asp Phe Pro Pro Ile Phe Trp Phe Cys Cys Ile  
 1 5 10 15

<210> 277  
 <211> 25  
 <212> PRT  
 <213> Conus miles

<400> 277  
 Glx Gly Phe Cys Cys Val Val Ile Pro Ile Leu Trp Phe Cys Cys Gly  
 1 5 10 15

Gly Tyr Arg Thr Asn Gly Thr Ala Asp  
 20 25

<210> 278  
 <211> 14  
 <212> PRT  
 <213> Conus vexillum

<400> 278  
 Phe Cys Cys Ile Phe Ala Pro Ile Leu Leu Phe Cys Cys Phe  
 1 5 10

<210> 279  
 <211> 45  
 <212> PRT  
 <213> Conus sulcatus

<400> 279  
 Glx Ser Gly Cys Arg Val Pro Phe Glu Leu Lys Cys Ile Trp Lys Phe  
 1 5 10 15  
 Cys Thr Ile Tyr Pro Ser Arg Pro Phe Ala Ser Leu Glu Glu Lys Asp  
 20 25 30  
 Glu Cys Gln Thr Val Thr Ile Thr Val Thr Trp Asp Phe  
 35 40 45

<210> 280  
 <211> 45  
 <212> PRT  
 <213> *Conus cinereus*

<400> 280  
 Ser Ser Gly Cys Ser Val Ser Leu Gly Phe Lys Cys Phe Trp Lys Ser  
 1 5 10 15  
 Cys Thr Val Ile Pro Val Arg Pro Phe Val Ser Leu Glu Glu Glu Asn  
 20 25 30  
 Glu Cys Gln Lys Val Gln Ile Ser Ala Val Trp Gly Pro  
 35 40 45

<210> 281  
 <211> 25  
 <212> PRT  
 <213> *Conus parius*

<400> 281  
 Pro Pro Phe Ser Cys Ser Gly Leu Arg Gly Gly Cys Val Leu Pro Pro  
 1 5 10 15  
 Asn Leu Arg Pro Lys Phe Asn Lys Gly  
 20 25

<210> 282  
 <211> 24  
 <212> PRT  
 <213> *Conus parius*

<400> 282  
 Pro Pro Phe Ser Cys Ala Gly Leu Arg Gly Gly Cys Val Leu Pro Pro  
 1 5 10 15  
 Asn Leu Arg Pro Lys Phe Lys Glu  
 20

<210> 283  
 <211> 29  
 <212> PRT  
 <213> *Conus wittigi*

<400> 283  
 Ser Ser Asp Gly Ser Asp Pro Lys Ala Lys Lys Gln Cys Met Trp Lys  
 1 5 10 15  
 Arg Cys Ile Pro Asp Gln Ser Arg Leu Glu Glu Asp Glu  
 20 25

<210> 284  
 <211> 30  
 <212> PRT  
 <213> *Conus cinereus*

<400> 284  
 Ser Ser Asp Gly Lys Ala Lys Lys Gln Cys Ala Trp Lys Thr Cys Val  
 1 5 10 15

Pro Thr Gln Trp Arg Arg Arg Asp Leu Lys Glu Lys Asp Glu  
                   20                  25                  30

<210> 285  
 <211> 30  
 <212> PRT  
 <213> Conus cinereus

<400> 285  
 Ser Ser Asp Gly Lys Ala Lys Arg Asn Cys Phe Trp Lys Ala Cys Val  
 1                  5                  10                  15

Pro Glu Gln Trp Arg Gln Arg Asp Pro Lys Glu Lys Asp Glu  
                   20                  25                  30

<210> 286  
 <211> 30  
 <212> PRT  
 <213> Conus cinereus

<400> 286  
 Ser Ser Asp Gly Lys Ala Lys Arg Asn Cys Phe Trp Lys Ala Cys Val  
 1                  5                  10                  15

Pro Glu Gln Trp Arg Gln Arg Asp Leu Lys Glu Lys Asp Glu  
                   20                  25                  30

<210> 287  
 <211> 37  
 <212> PRT  
 <213> Conus nobilis

<400> 287  
 Phe Arg Pro Ala Val Lys Ser Arg Ser Arg Arg Ala Pro Pro Cys Val  
 1                  5                  10                  15

Trp Lys Val Cys Pro Ala Pro Pro Trp Leu Val Thr Lys Arg Lys Gln  
                   20                  25                  30

Glu Thr Ser Asp Tyr  
                   35

<210> 288  
 <211> 37  
 <212> PRT  
 <213> Conus nobilis

<400> 288  
 Phe Arg Pro Ala Val Lys Ser Arg Ser Arg Arg Ala Pro Pro Cys Val  
 1                  5                  10                  15

Trp Lys Val Cys Pro Ala Pro Pro Trp Leu Val Thr Lys Arg Lys Gln  
                   20                  25                  30

Glu Thr Ser Asp Tyr  
                   35

<210> 289  
 <211> 37  
 <212> PRT

<213> *Conus miles*

<400> 289

Phe Arg Pro Ala Met Gln Ser Arg Ser Gly Gly Met Ser Leu Cys Leu  
1 5 10 15

Trp Lys Val Cys Pro Ala Ala Pro Trp Leu Val Ala Lys Arg Lys Gln  
20 25 30

Glu Thr Ser Asp Tyr  
35

<210> 290

<211> 21

<212> PRT

<213> *Conus tulipa*

<400> 290

His Phe Asn Ser Val Val Pro Thr Val Tyr Ile Cys Met Trp Lys Val  
1 5 10 15

Cys Pro Pro Ser Pro  
20

<210> 291

<211> 21

<212> PRT

<213> *Conus purpurascens*

<400> 291

Glx Ser Glu Glu Glu Lys Ile Cys Leu Trp Lys Ile Cys Pro Pro Pro  
1 5 10 15

Pro Trp Arg Arg Ser  
20

<210> 292

<211> 21

<212> PRT

<213> *Conus purpurascens*

<400> 292

Glu Ser Asn Gly Val Glu Ile Cys Met Trp Lys Val Cys Pro Pro Ser  
1 5 10 15

Pro Trp Arg Arg Ser  
20

<210> 293

<211> 38

<212> PRT

<213> *Conus vexillum*

<400> 293

Ile Met Gln Ser Leu Val Phe Ser His Gln Pro Leu Pro Thr Ala Ser  
1 5 10 15

Ile Cys Ile Trp Lys Ile Cys Pro Pro Asp Pro Trp Arg Arg His Asp  
20 25 30

Leu Gln Lys Ser Asn Lys  
35

<210> 294  
<211> 38  
<212> PRT  
<213> Conus muriculatus

<400> 294  
Ile Met Gln Ser Leu Val Phe Ser His Gln Pro Leu Pro Thr Ala Ser  
1 5 10 15

Ile Cys Ile Trp Lys Ile Cys Pro Pro Asp Pro Trp Arg Arg His Asp  
20 25 30

Leu Gln Lys Ser Asn Lys  
35

<210> 295  
<211> 26  
<212> PRT  
<213> Conus pulicarius

<400> 295  
Val Arg Leu Arg Gly Gln Ile Cys Ile Trp Lys Val Cys Pro Pro Leu  
1 5 10 15

Leu Gln Trp Ile His Pro Leu Val Lys Arg  
20 25

<210> 296  
<211> 26  
<212> PRT  
<213> Conus pulicarius

<400> 296  
Val Arg Pro Arg Gly Gln Ile Cys Ile Trp Lys Val Cys Pro Pro Leu  
1 5 10 15

Leu Gln Trp Ile His Pro Leu Val Lys Arg  
20 25

<210> 297  
<211> 27  
<212> PRT  
<213> Conus pulicarius

<400> 297  
Pro Val Arg Leu Arg Gly Gln Ile Cys Ile Trp Lys Val Cys Pro Pro  
1 5 10 15

Leu Leu Gln Trp Ile His Pro Leu Val Lys Arg  
20 25

<210> 298  
<211> 30  
<212> PRT  
<213> Conus mustelinus

<400> 298



Leu Val Ser His Thr Ser Ser Lys Tyr Pro Gly Val Thr Phe Cys Pro  
 1 5 10 15

Trp Lys Val Cys Pro Pro Ala Pro Trp Arg Ile Leu Gly Val  
 20 25 30

<210> 299  
 <211> 22  
 <212> PRT  
 <213> *Conus baileyi*

<400> 299  
 His Ser Asp Ser Ile Ile Leu Arg Gly Leu Cys Ile Trp Lys Val Cys  
 1 5 10 15

Glu Pro Pro Pro Gln Arg  
 20

<210> 300  
 <211> 26  
 <212> PRT  
 <213> *Conus planorbis*

<400> 300  
 Ser Ser Ser Asn Gly Leu Lys Arg Ala Asp Leu Cys Ile His Lys Ile  
 1 5 10 15

Cys Pro Pro Arg Tyr His Gln Ser Gln Gln  
 20 25

<210> 301  
 <211> 36  
 <212> PRT  
 <213> *Conus litteratus*

<400> 301  
 His Arg Val Phe His Leu Asp Asn Thr Tyr Leu Lys Ile Pro Ile Cys  
 1 5 10 15

Ala Trp Lys Val Cys Pro Pro Thr Pro Trp Arg Arg Arg Asp Leu Lys  
 20 25 30

Lys Arg Asn Lys  
 35

<210> 302  
 <211> 50  
 <212> PRT  
 <213> *Conus litteratus*

<400> 302  
 Ser Pro Val Ser Thr Pro Tyr Pro Glu Phe His Leu Asp Glu Pro Tyr  
 1 5 10 15

Leu Lys Ile Pro Val Cys Ile Trp Lys Ile Cys Pro Pro Asn Leu Leu  
 20 25 30

Arg Arg Arg Asp Leu Lys Lys Arg Asn Lys Val Arg Gln Thr Thr Ala  
 35 40 45

Thr Thr  
50

<210> 303  
<211> 26  
<212> PRT  
<213> Conus coronatus

<400> 303  
Leu Ser Asp Gly Arg Asp Trp Thr Gly Tyr Ile Cys Ile Trp Lys Ala  
1 5 10 15

Cys Pro Arg Pro Trp Ile Pro Pro Lys  
20 25

<210> 304  
<211> 29  
<212> PRT  
<213> Conus chaldaeus

<400> 304  
Leu Ser Glu Gly Arg Asn Ser Thr Val His Ile Cys Met Trp Lys Val  
1 5 10 15

Cys Pro Pro Pro Pro Trp Arg Arg Pro His Gly Gln Arg  
20 25

<210> 305  
<211> 29  
<212> PRT  
<213> Conus chaldaeus

<400> 305  
Leu Ser Glu Gly Arg Asn Ser Thr Val His Ile Cys Thr Trp Lys Val  
1 5 10 15

Cys Pro Pro Pro Pro Trp Arg Arg Pro His Gly Gln Arg  
20 25

<210> 306  
<211> 13  
<212> PRT  
<213> Unknown

<220>  
<223> unknown Conus species

<400> 306  
Glx Cys Met Trp Lys Arg Cys Ile Pro Asp Gln Ser Arg  
1 5 10

<210> 307  
<211> 15  
<212> PRT  
<213> Unknown

<220>  
<223> unknown Conus species

<400> 307  
Val Asp Ile Cys Asn Trp Arg Ile Cys Ala Pro Asn Pro Leu Arg

## 123

1                      5                      10                      15

<210> 308  
 <211> 13  
 <212> PRT  
 <213> Conus geographus

<220>  
 <221> PEPTIDE  
 <222> (1)..(13)  
 <223> Xaa may be Trp (D or L)

<400> 308  
 Leu Cys Phe Xaa Lys Ser Cys Arg Pro Tyr Pro Trp Arg  
 1                      5                      10

<210> 309  
 <211> 16  
 <212> PRT  
 <213> Conus magus

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa may be Trp (D or L)

<400> 309  
 Leu Phe Cys Phe Xaa Trp Lys Ser Cys Trp Pro Arg Pro Tyr Trp Arg  
 1                      5                      10                      15

<210> 310  
 <211> 16  
 <212> PRT  
 <213> Conus magus

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa may be Trp (D or L)

<400> 310  
 Leu Phe Cys Phe Xaa Lys Ser Cys Trp Pro Arg Pro Tyr Pro Trp Arg  
 1                      5                      10                      15

<210> 311  
 <211> 15  
 <212> PRT  
 <213> Conus magus

<220>  
 <221> PEPTIDE  
 <222> (1)..(15)  
 <223> Xaa may be Phe (D or L)

<400> 311  
 Leu Xaa Cys Phe Trp Lys Ser Cys Trp Pro Arg Pro Tyr Trp Arg  
 1                      5                      10                      15

<210> 312  
 <211> 15

<212> PRT  
 <213> Conus magus  
  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(15)  
 <223> Xaa at residue 2 may be Phe (D or L); Xaa at residue 5 may be Trp  
 (D or L)  
  
 <400> 312  
 Leu Xaa Cys Phe Xaa Lys Ser Cys Trp Pro Arg Pro Tyr Trp Arg  
 1 5 10 15  
  
 <210> 313  
 <211> 11  
 <212> PRT  
 <213> Conus magus  
  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(11)  
 <223> Xaa may be Phe (D or L)  
  
 <400> 313  
 Leu Xaa Cys Phe Trp Lys Ser Cys Trp Pro Arg  
 1 5 10  
  
 <210> 314  
 <211> 11  
 <212> PRT  
 <213> Conus magus  
  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(11)  
 <223> Xaa may be Trp (D or L)  
  
 <400> 314  
 Leu Phe Cys Phe Xaa Lys Ser Cys Trp Pro Arg  
 1 5 10  
  
 <210> 315  
 <211> 11  
 <212> PRT  
 <213> Conus magus  
  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(11)  
 <223> Xaa at residue 2 may be Phe (D or L); Xaa at residue 5 may be Trp  
 (D or L)  
  
 <400> 315  
 Leu Xaa Cys Phe Xaa Lys Ser Cys Trp Pro Arg  
 1 5 10  
  
 <210> 316  
 <211> 9  
 <212> PRT  
 <213> Conus magus

```

<220>
<221> PEPTIDE
<222> (1)..(9)
<223> Xaa may be Phe (D or L)
<400> 316
Leu Xaa Cys Phe Trp Lys Ser Cys Trp
1          5

<210> 317
<211> 9
<212> PRT
<213> Conus magus

<220>
<221> PEPTIDE
<222> (1)..(9)
<223> Xaa may be Trp (D or L)

<400> 317
Leu Phe Cys Phe Xaa Lys Ser Cys Trp
1          5

<210> 318
<211> 9
<212> PRT
<213> Conus magus

<220>
<221> PEPTIDE
<222> (1)..(9)
<223> Xaa at residue 2 may be Phe (D or L); Xaa at residue 5 may be Trp
      (D or L)

<400> 318
Leu Xaa Cys Phe Xaa Lys Ser Cys Trp
1          5

<210> 319
<211> 10
<212> PRT
<213> Conus magus

<220>
<221> PEPTIDE
<222> (1)..(10)
<223> Xaa may be Trp (D or L)

<400> 319
Phe Cys Phe Xaa Lys Ser Cys Trp Pro Arg
1          5          10

<210> 320
<211> 10
<212> PRT
<213> Conus magus

<220>
<221> PEPTIDE
<222> (1)..(10)

```

<223> Xaa may be Lys (D or L)

<400> 320

Phe Cys Phe Trp Xaa Ser Cys Trp Pro Arg  
1 5 10

<210> 321

<211> 10

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(10)

<223> Xaa may be Trp (D or L)

<400> 321

Phe Cys Phe Xaa Phe Ser Cys Trp Pro Arg  
1 5 10

<210> 322

<211> 10

<212> PRT

<213> Conus magus

<400> 322

Phe Cys Phe Trp Lys Ser Cys Trp Pro Arg  
1 5 10

<210> 323

<211> 21

<212> PRT

<213> Conus purpurascens

<220>

<221> PEPTIDE

<222> (1)..(21)

<223> Xaa may be Trp (D or L)

<400> 323

Glu Ser Asn Gly Val Glu Ile Cys Met Xaa Lys Val Cys Pro Pro Ser  
1 5 10 15

Pro Trp Arg Arg Ser  
20

<210> 324

<211> 14

<212> PRT

<213> Conus striatus

<220>

<221> PEPTIDE

<222> (1)..(14)

<223> Xaa may be Trp (D or L)

<400> 324

Met Glu Cys Tyr Xaa Lys Ala Cys Arg Pro Thr Leu Ser Arg  
1 5 10

<210> 325  
 <211> 16  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa may be Trp (D or L)

<400> 325  
 Phe Glu Leu Lys Cys Ile Xaa Lys Phe Cys Thr Ile Tyr Pro Ser Arg  
 1 5 10 15

<210> 326  
 <211> 18  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(18)  
 <223> Xaa may be Trp (D or L)

<400> 326  
 Phe Glu Leu Lys Cys Ile Xaa Lys Phe Cys Thr Ile Tyr Pro Ser Arg  
 1 5 10 15

Pro Phe

<210> 327  
 <211> 14  
 <212> PRT  
 <213> Conus tulipa

<220>  
 <221> PEPTIDE  
 <222> (1)..(14)  
 <223> Xaa may be Trp (D or L)

<400> 327  
 Thr Val Tyr Ile Cys Met Xaa Lys Val Cys Pro Pro Ser Pro  
 1 5 10

<210> 328  
 <211> 22  
 <212> PRT  
 <213> Conus aurisiacus

<220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa may be Trp (D or L)

<400> 328  
 Ser Asp Ser Ser Asp Gln Lys Ala Gln Ile Cys Ile Xaa Lys Val Cys  
 1 5 10 15

Pro Pro Pro Pro Trp Arg  
 20

<210> 329  
 <211> 16  
 <212> PRT  
 <213> Conus consors

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa may be Trp (D or L)

<400> 329  
 Gly Ala Gln Ile Cys Ile Xaa Lys Val Cys Pro Pro Ser Pro Trp Arg  
 1 5 10 15

<210> 330  
 <211> 30  
 <212> PRT  
 <213> Conus musicus

<220>  
 <221> PEPTIDE  
 <222> (1)..(30)  
 <223> Xaa may be Trp (D or L)

<400> 330  
 Met Phe Pro Ser Leu Ala Leu Gly Pro Gly Gly Asp Val Ile Cys Arg  
 1 5 10 15

Xaa Lys Val Cys Pro Pro Thr Pro Trp Lys Arg Leu Ile Lys  
 20 25 30

<210> 331  
 <211> 24  
 <212> PRT  
 <213> Conus flavidus

<220>  
 <221> PEPTIDE  
 <222> (1)..(24)  
 <223> Xaa may be Trp (D or L)

<400> 331  
 Val Asp Ile Cys Asn Xaa Arg Ile Cys Ala Pro Asn Pro Leu Arg Arg  
 1 5 10 15

His Asp Leu Lys Lys Gly Asn Asn  
 20

<210> 332  
 <211> 15  
 <212> PRT  
 <213> Conus flavidus

<220>  
 <221> PEPTIDE  
 <222> (1)..(15)  
 <223> Xaa may be Trp (D or L)

<400> 332



Val Asp Ile Cys Asn Xaa Arg Ile Cys Ala Pro Asn Pro Leu Arg  
 1 5 10 15

<210> 333  
 <211> 22  
 <212> PRT  
 <213> Conus geographus

<220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa may be Trp (D or L)

<400> 333  
 Arg Leu Phe Cys Phe Xaa Lys Ser Cys Thr Trp Arg Pro Tyr Pro Trp  
 1 5 10 15

Arg Arg Arg Asp Leu Asn  
 20

<210> 334  
 <211> 17  
 <212> PRT  
 <213> Conus generalis

<220>  
 <221> DISULFID  
 <222> (4)..(14)

<400> 334  
 Ser Leu Trp Cys Val Cys Pro Phe Arg Val Cys Pro Pro Cys His Gly  
 1 5 10 15

Arg

<210> 335  
 <211> 17  
 <212> PRT  
 <213> Conus generalis

<220>  
 <221> DISULFID  
 <222> (6)..(14)

<400> 335  
 Ser Leu Trp Cys Val Cys Pro Phe Arg Val Cys Pro Pro Cys His Gly  
 1 5 10 15

Arg

<210> 336  
 <211> 15  
 <212> PRT  
 <213> Conus generalis

<220>  
 <221> PEPTIDE  
 <222> (1)..(15)  
 <223> Xaa may be Phe (D or L)

<220>  
 <221> DISULFID  
 <222> (4)..(14)

<400> 336  
 Ser Leu Trp Cys Val Cys Pro Xaa Arg Val Cys Pro Pro Cys His  
 1 5 10 15

<210> 337  
 <211> 15  
 <212> PRT  
 <213> *Conus generalis*

<220>  
 <221> PEPTIDE  
 <222> (1)..(15)  
 <223> Xaa may be Phe (D or L)

<220>  
 <221> DISULFID  
 <222> (6)..(14)

<400> 337  
 Ser Leu Trp Cys Val Cys Pro Xaa Arg Val Cys Pro Pro Cys His  
 1 5 10 15

<210> 338  
 <211> 6  
 <212> PRT  
 <213> *Conus magus*

<220>  
 <221> PEPTIDE  
 <222> (1)..(6)  
 <223> Xaa at residues 2 and 5 may be any amino acid; Xaa at residue 3 may be Trp (D or L) or bromo-Trp (D or L)

<400> 338  
 Cys Xaa Xaa Lys Xaa Cys  
 1 5

<210> 339  
 <211> 6  
 <212> PRT  
 <213> *Conus generalis*

<220>  
 <221> PEPTIDE  
 <222> (1)..(6)  
 <223> Xaa may be Phe (D or L)

<400> 339  
 Cys Pro Xaa Arg Val Cys  
 1 5

<210> 340  
 <211> 21  
 <212> PRT  
 <213> *Conus ebraeus*

&lt;400&gt; 340

Leu Ser Gly Gly Thr Tyr Ser Arg Val Asp Thr Cys Ile Trp Lys Val  
1 5 10 15

Cys Pro Gln Ser Pro  
20